

# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 05-28-03  
Searcher: Reveling E4952  
Terminal time: 20  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 25  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

Search Site  
\_\_\_\_\_ STIC  
\_\_\_\_\_ CM-1  
\_\_\_\_\_ Pre-S  
Type of Search  
\_\_\_\_\_ N.A. Sequence  
\_\_\_\_\_ A.A. Sequence  
\_\_\_\_\_ Structure  
\_\_\_\_\_ Bibliographic

Vendors  
\_\_\_\_\_ IG Suite  
\_\_\_\_\_ STN  
\_\_\_\_\_ Dialog  
\_\_\_\_\_ APS  
\_\_\_\_\_ Geninfo  
\_\_\_\_\_ SDC  
\_\_\_\_\_ DARC/Questel  
\_\_\_\_\_ Other CGN

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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2003, 18:02:22 ; Search time 1902 Seconds

(without alignments)  
4911.672 Million cell updates/sec

Title: US-09-930-312-1  
Sequence: 1 ggtggaactgctgctt.....acttttaagacaagtg 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_da:\*  
2: gb\_hlg:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	321	100.0	321	6	AX384516
2	321	100.0	1068	6	AX148176
3	321	100.0	2049	6	AX385037
4	321	100.0	2142	6	AX451566
5	321	100.0	2193	6	AX385032
6	321	100.0	2214	6	AX451562
7	321	100.0	2265	6	AX385027
8	321	100.0	2436	9	AF453828
9	321	100.0	2838	9	AF403384
10	321	100.0	2838	9	AF403384
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## ALIGNMENTS

RESULT 1  
AX384516  
LOCUS  
DEFINITION  
Sequence 1 from Patent WO0214496.  
ACCESSION  
AX384516  
VERSION  
AX384516.1 GI:19577719  
KEYWORDS  
SOURCE  
human.  
ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Lind, P.  
Novel g protein-coupled receptors  
Patent: WO 0214496-A 1 21-FEB-2002.

PHARMACIA & UPJOHN COMPANY (US)  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 76 a 67 c 59 g 119 t  
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Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 ATTCAAAAACCGCTTGCAGACACAGAGTAAGAAATGTTTGGAGAGAGTGGCT 120  
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DB 121 GTTCAAAATCGTTTCTTTTATAGTCTCTGATGCAATGCTGATCTGTAATT 180  
OY 181 GTAGTAAATCGTTTCCCTCCGCTCCGCGTGAATACGACACAATGACTTCTGATA 240  
DB 181 GTAGTAAATCGTTTCCCTCCCTCCGCGGGAATACGACACAATGACTTCTGATA 240  
OY 241 GTGATTTTTCCTTCAGTTAAACAGTCTTTGAATCAATGCTCTATCTCACAAC 300  
DB 241 GTGATTTTTCCTTCAGTTAAACAGTCTTTGAATCAATGCTCTATCTCACAAC 300  
OY 301 AACTTTTAAAGACAGTTG 321  
DB 301 AACTTTTAAAGACAGTTG 321

## RESULT 2

AX148176 1068 bp DNA linear PAT 08-JUN-2001  
LOCUS AX148176  
DEFINITION Sequence 17 from Patent WO0136471.  
ACCESSION AX148176  
VERSION AX148176.1 GI:14347081  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1068)  
AUTHORS Chen, R., Dang, H., and Lowitz, K.P.  
TITLE Endogenous and non-endogenous versions of human g protein-coupled receptors  
JOURNAL Patent: WO 0136471-A 17 25-MAY-2001;  
Arena Pharmaceuticals, Inc. (US)  
Location/Qualifiers

FEATURES  
source 1. .1068  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 278 a 215 c 214 g 361 t  
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Query Match 100.0%; Score 321; DB 6; Length 1068;  
Best Local Similarity 100.0%; Pred. No. 5.7e-71;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 589 GGTGGAACCTGCTGGCTTTTCATCATGTTGTTTCTATATCTATATGTTCTGTC 648  
OY 61 ATTCAAAAACCGCTTGCAGACACAGAGTAAGAAATGTTTGGAGAGAGTGGCT 120  
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OY 121 GTTCAAAATCGTTTCTTTTATAGTCTCTGATGCCATCTGCTGATCTCTGTAATT 180  
DB 709 GTTCAAAATCGTTTCTTTTATAGTCTCTGATGCCATCTGCTGATCTCTGTAATT 768  
OY 181 GTAGTAAATCGTTTCCCTCCGCTCCGCGTGAATACGACACAAATGACTTCTGATA 240  
DB 769 GTAGTAAATCGTTTCCCTCCGCTCCGCGGGAATACGACACAAATGACTTCTGATA 828  
OY 241 GTGATTTTTCCTTCAGTTAAACAGTCTTTGAATCAATGCTCTATATCTCACAAC 300  
DB 829 GTGATTTTTCCTTCAGTTAAACAGTCTTTGAATCAATGCTCTATATCTCACAAC 888  
OY 301 AACTTTTAAAGACAGTTG 321  
DB 889 AACTTTTAAAGACAGTTG 909

## RESULT 3

AX385037 2049 bp DNA linear PAT 19-MAR-2002  
LOCUS AX385037  
DEFINITION Sequence 11 from Patent WO0214489.  
ACCESSION AX385037  
VERSION AX385037.1 GI:19578160  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1  
AUTHORS Paszty, C.J., Gong, J., Daugherty, B. and Rogers, N.  
TITLE Leucine-rich repeat-containing g-protein coupled receptor-8  
JOURNAL Patent: WO 0214489-A 11 21-FEB-2002;  
Amgen, Inc. (US)  
Location/Qualifiers

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BASE COUNT 579 a 415 c 395 g 660 t  
ORIGIN

Query Match 100.0%; Score 321; DB 6; Length 2049;  
Best Local Similarity 100.0%; Pred. No. 5.3e-71;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTGGAACCTGCTGGCTTTTCATCATGTTGTTTCTATATCTATATGTTCTGTC 60  
DB 1570 GGTGGAACCTGCTGGCTTTTCATCATGTTGTTTCTATATCTATATGTTCTGTC 1629  
OY 61 ATTCAAAAACCGCTTGCAGACACAGAGTAAGAAATGTTTGGAGAGAGTGGCT 120  
DB 1630 ATTCAAAAACCGCTTGCAGACACAGAGTAAGAAATGTTTGGAGAGAGTGGCT 1689  
OY 121 GTTCAAAATCGTTTCTTTTATAGTCTCTGATGCCATCTGCTGATCTCTGTAATT 180



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Db 1690 GTTGAACATCGTTCTTTTATAGTGTCTGATGCCATCGTGATGATCTGATTT 1749  
QY 181 GTAGTAAATCGTTCTTCCCTTCGCGGTGAATACGACACATGATCTCTGGATA 240  
Db 1750 GTAGTAAATCGTTCTTCCCTTCGCGGTGAATACGACACATGATCTCTGGATA 1809  
QY 241 GTGATTTTTCCTTCAGTTAAGAGTGTGTAATCCATCTCTATCTCTCACACCC 300  
Db 1810 GTGATTTTTCCTTCAGTTAAGAGTGTGTAATCCATCTCTATCTCTCACACCC 1869  
QY 301 AACTTTTAAAGACAAGTTG 321  
Db 1870 AACTTTTAAAGACAAGTTG 1890

RESULT 4  
AX451566 2142 bp DNA linear PAT 03-JUL-2002  
LOCUS AX451566  
DEFINITION Sequence 5 from Patent WO0226824.  
ACCESSION AX451566  
VERSION AX451566.1 GI:21698550  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
1 Feder, J.N., Mintler, G., Ramanathan, C.S. and Hawken, D.R.  
A novel human g-protein coupled receptor, hgrbm5, expressed  
highly in brain and ovarian tissues  
Patent: WO 0226824-A 5 04-APR-2002;  
Bristol-Myers Squibb Company (US)

JOURNAL  
location/Qualifiers  
FEATURES  
Source 1..2142  
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/db\_xref="taxon:9606"  
BASE COUNT 613 a 435 c 408 g 686 t  
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Query Match 100.0%; Score 321; DB 6; Length 2142;  
Best Local Similarity 100.0%; Pred. No. 5.3e-71;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1663 GGTGGAACCTGCTGCTTTCTCATCATGTTGTTTCCATATATCTATGTTGTTCC 1722  
QY 61 ATTCAAAAACCGCTTCGACACACAGAAAGTAAGAAATGTTTGGAGAGAGGTGCT 120  
Db 1723 ATTCAAAAACCGCTTCGACACACAGAAAGTAAGAAATGTTTGGAGAGAGGTGCT 1782  
QY 121 GTTGAATCGTTCTTTTATAGTGTCTGATGCCATCTGCTGATTTCTCTATTT 180  
Db 1783 GTTGAATCGTTCTTTTATAGTGTCTGATGCCATCTGCTGATTTCTCTATTT 1842  
QY 181 GTAGTAAATCGTTCTTCCCTTCGCGGTGAATACGACACATGATCTCTGGATA 240  
Db 1843 GTAGTAAATCGTTCTTCCCTTCGCGGTGAATACGACACATGATCTCTGGATA 1902  
QY 241 GTGATTTTTCCTTCAGTTAAGAGTGTGTAATCCATCTCTATCTCTCACACCC 300  
Db 1903 GTGATTTTTCCTTCAGTTAAGAGTGTGTAATCCATCTCTATCTCTCACACCC 1962  
QY 301 AACTTTTAAAGACAAGTTG 321  
Db 1963 AACTTTTAAAGACAAGTTG 1983

RESULT 5  
AX385032 2193 bp DNA linear PAT 19-MAR-2002  
LOCUS AX385032  
DEFINITION Sequence 6 from Patent WO0214489.

ACCESSION AX385032  
VERSION AX385032.1 GI:19578156  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
1 Paszty, C.J., Gong, J., Daugherty, B. and Rogers, N.  
Leucine-rich repeat-containing g-protein coupled receptor-8  
molecules and uses thereof  
Patent: WO 0214489-A 6 21-FEB-2002;  
Amgen, Inc. (US)

JOURNAL  
location/Qualifiers  
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PGKROTSVILICIMAGFLVIVPFMKDYGNGFNKNGVCFPLXYOTEDISGKGS  
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Query Match 100.0%; Score 321; DB 6; Length 2193;  
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Db 1894 GTAGTAAATCGTTCTTCCCTTCGCGGTGAATACGACACATGATCTCTGGATA 1953  
QY 241 GTGATTTTTCCTTCAGTTAAGAGTGTGTAATCCATCTCTATCTCTCACACCC 300  
Db 1954 GTGATTTTTCCTTCAGTTAAGAGTGTGTAATCCATCTCTATCTCTCACACCC 2013  
QY 301 AACTTTTAAAGACAAGTTG 321  
Db 2014 AACTTTTAAAGACAAGTTG 2034

RESULT 6  
AX451562 2214 bp DNA linear PAT 03-JUL-2002  
LOCUS AX451562  
DEFINITION Sequence 1 from Patent WO0226824.  
ACCESSION AX451562

VERSION AX451562.1 GI:21698547  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Feder, J.N., Mintier, G., Ramanathan, C.S. and Hawken, D.R.  
TITLE A novel human g-protein coupled receptor, hgrbm5, expressed highly in brain and ovarian tissues  
JOURNAL Patent: WO 026824-A 1 04-APR-2002;  
Bristol-Myers Squibb Company (us)  
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source location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 5.2e-71;  
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Db 1915 GTAGTAAATCCTTCCCTTCCTCGGGTGAATAATACAGACAGAAATGCTTCTGATA 1974

QY 241 GTGATTTTTTCTTCCAGTTAAACAGTCTTGAATCCATCCCTATACCTCACAAC 300  
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Db 1975 GTGATTTTTTCTTCCAGTTAAACAGTCTTGAATCCATCCCTATACCTCACAAC 2034

QY 301 AACTTTTTTAAGACAAGTTG 321  
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Db 2035 AACTTTTTTAAGACAAGTTG 2055

RESULT 7  
AX385027 2265 bp DNA Linear PAT 19-MAR-2002  
LOCUS AX385027  
DEFINITION Sequence 1 from Patent W00214489.  
ACCESSION AX385027  
VERSION AX385027.1 GI:19578152  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Paszty, C.J., Gong, J., Daugherty, B. and Rogers, N.  
TITLE Leucite-rich repeat-containing g-protein coupled receptor-8 molecules and uses thereof  
JOURNAL Patent: WO 0214489-A 1 21-FEB-2002;  
Amgen, Inc. (US)  
FEATURES  
source location/Qualifiers  
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/db\_xref="GI:19578153"  
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QY 1 GGTGTAACCTGCTGGCTTTCTCATCATGTTGTTTCTATATATATGTTCTGTTCC 60  
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Db 1786 GGTGTAACCTGCTGGCTTTCTCATCATGTTGTTTCTATATATATGTTCTGTTCC 1845

QY 61 ATTCAAAAACCGCTTCGACAGACAGAGTAAGAAATGTTTGGAGAGAGTGCT 120  
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Db 1846 ATTCAAAAACCGCTTCGACAGACAGAGTAAGAAATGTTTGGAGAGAGTGCT 1905

QY 121 GTTCAAAATGTTTCTTTTATAGTGTCTCTGATGCAATGCTGATGCTGATTT 180  
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Db 1906 GTTCAAAATGTTTCTTTTATAGTGTCTCTGATGCAATGCTGATGCTGATTT 1965

QY 181 GTAGTAAATCCTTCCCTTCCTCGGGTGAATAATACAGACAGAAATGCTTCTGATA 240  
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Db 1966 GTAGTAAATCCTTCCCTTCCTCGGGTGAATAATACAGACAGAAATGCTTCTGATA 2025

QY 241 GTGATTTTTTCTTCCAGTTAAACAGTCTTGAATCCATCCCTATACCTCACAAC 300  
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Db 2026 GTGATTTTTTCTTCCAGTTAAACAGTCTTGAATCCATCCCTATACCTCACAAC 2085

QY 301 AACTTTTTTAAGACAAGTTG 321  
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Db 2086 AACTTTTTTAAGACAAGTTG 2106

RESULT 8  
AF453828 2436 bp mRNA Linear PRI 04-FEB-2002  
LOCUS AF453828  
DEFINITION Homo sapiens g protein-coupled receptor affecting testicular  
descent (GREAT) mRNA, complete cds.  
ACCESSION AF453828  
VERSION AF453828.1 GI:18483167  
KEYWORDS Homo sapiens.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2436)  
AUTHORS Gorlov, I.P., Kanat, A., Jones, E., Lamb, D., Truong, A., Bogatcheva, N., Bishop, C.E., McElravey, K. and Agoulnik, A.I.  
TITLE Mutations of the GREAT gene cause cryptorchidism  
JOURNAL Unpublished  
AUTHORS Agoulnik, A.I.  
TITLE Direct Submission  
JOURNAL Submitted (30-NOV-2001) Db/Gyn, Baylor College of Medicine, 6550 Fannin St., Su. 861, Houston, TX 77030, USA  
FEATURES  
source location/Qualifiers  
1..2436  
/organism="Homo sapiens"

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/db_xref="taxon:9606"
/chromosome="13"
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1..2436
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71..2335
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TKKKIFLHNCIHRISRKAFPGICNLIILNHCITTLRPGIFKDLHDTLID
NPIRISORLFTGLNSLPFLSMVNNYLEALPKQCAQMPOLNWDLSBNKIKYLTNT
FLSCDSLTVLFLPNQIGVEPEKTFSSLNIGELSSNTITELSPHLFKDLKLOL
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APHYRICMPLTDGISSEDLANNILRIFWAVAFICFQNLFIYIGMRSFKANTH
AMSIKILCCADCLMGVYLFVGIIDIRGOYKALIMMESVOCRLMGFLAMSTEV
SVLLTFLTELEKFLVIFPPSNIIRGKROTSVILICIMAGFLIAYIPENKDYFGE
YKNGVCEPLIYDQTEDEIGSKYSLGIFLVNLAFLIYVSTITMCSIOKRLQTT
EVNRCFGEVAVANRFEIVFSDAICWIPVAVVILSLFVEIPDITMSVIFELPV
NSALNPLIYLTITNFEFKDLKQLLHKHQRKSIKIKKSLSTSIWIEDSSSLKGLV
NKITLGDSSIMKPVs"

BASE COUNT      703 a      503 c      456 g      774 t
ORIGIN

Query Match      100.0%; Score 321; DB 9; Length 2436;
Best Local Similarity 100.0%; Pred. No. 5.2e-71;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGGAACCTGCGCTTTCTCATCATGTGTTTCCATATACATATGCTGTTCC 60
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DB 1856 GGTGGAACCTGCGCTTTCTCATCATGTGTTTCCATATACATATGCTGTTCC 1915

QY 61 ATTCAAAAACCGCCTTCGACAGCACAGAAAGTGAAGTGTGTTTGAAGAGAGTGCT 120
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DB 1916 ATTCAAAAACCGCCTTCGACAGCACAGAAAGTGAAGTGTGTTTGAAGAGAGTGCT 1975

QY 121 GTTGAATTCGTTTCTTTTATAGTGTCTCTGATGCCATCTGCTGATTCCTATATT 180
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DB 1976 GTTGAATTCGTTTCTTTTATAGTGTCTCTGATGCCATCTGCTGATTCCTATATT 2035

QY 181 GTAGTAAATACCTTCCCTCTTCGCGGTGAATAATACACACATACATCTCGGATA 240
    |||||
DB 2036 GTAGTAAATACCTTCCCTCTTCGCGGTGAATAATACACACATACATCTCGGATA 2095

QY 241 GTGATTTTTTCTTCGAGTTAACAGTCTTTGAATCCATCTCTATCTCACAACC 300
    |||||
DB 2096 GTGATTTTTTCTTCGAGTTAACAGTCTTTGAATCCATCTCTATCTCACAACC 2155

QY 301 AACTTTTAAAGACAAGTTG 321
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DB 2156 AACTTTTAAAGACAAGTTG 2176

RESULT 9
AF403384      2838 bp      mRNA      linear      PRI 19-FEB-2002
DEFINITION   Homo sapiens LGR8 mRNA, complete cds.
ACCESSION   AF403384
VERSION      AF403384.2 GI:18702459
KEYWORDS
SOURCE       Homo sapiens.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1 (bases 1 to 2838)
AUTHORS     Hsu,S.Y., Nakabayashi,K., Nishi,S., Kunagai,J., Kudo,M.,
Sherwood,O.D. and Hsueh,A.J.
TITLE       Activation of orphan receptors by the hormone relaxin

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JOURNAL      Science 295 (5555), 671-674 (2002)
MEDLINE      21669315
PUBMED       11809971
REFERENCE    2 (bases 1 to 2838)
AUTHORS     Hsu,S.Y., Nakabayashi,K. and Bhalla,A.
TITLE       Direct Submission
JOURNAL      Submitted (26-JUL-2001) GYN/OB, Stanford University, MSOB 5385,
Stanford, CA 94305, USA
REFERENCE    3 (bases 1 to 2838)
AUTHORS     Hsueh,A.J.W.
TITLE       Direct Submission
JOURNAL      Submitted (19-FEB-2002) Division of Reproductive Biology,
Department of Gynecology and Obstetrics, Stanford University
Medical Center, 300 Pasteur Drive, Room A-344, Stanford, CA
94305-5317, USA
REMARK       Sequence update by submitter
COMMENT      On Feb 19, 2002 this sequence version replaced gi:18419431.
FEATURES
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/chromosome="11"
/map="11q13"
107..2371
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TKKKIFLHNCIHRISRKAFPGICNLIILNHCITTLRPGIFKDLHDTLID
NPIRISORLFTGLNSLPFLSMVNNYLEALPKQCAQMPOLNWDLSBNKIKYLTNT
FLSCDSLTVLFLPNQIGVEPEKTFSSLNIGELSSNTITELSPHLFKDLKLOL
NLSSNPLMLHKNQESLQKQSLDLERIEIPNITRMFQPMKNLSHYFNKRYCSY
APHYRICMPLTDGISSEDLANNILRIFWAVAFICFQNLFIYIGMRSFKANTH
AMSIKILCCADCLMGVYLFVGIIDIRGOYKALIMMESVOCRLMGFLAMSTEV
SVLLTFLTELEKFLVIFPPSNIIRGKROTSVILICIMAGFLIAYIPENKDYFGE
YKNGVCEPLIYDQTEDEIGSKYSLGIFLVNLAFLIYVSTITMCSIOKRLQTT
EVNRCFGEVAVANRFEIVFSDAICWIPVAVVILSLFVEIPDITMSVIFELPV
NSALNPLIYLTITNFEFKDLKQLLHKHQRKSIKIKKSLSTSIWIEDSSSLKGLV
NKITLGDSSIMKPVs"

BASE COUNT      817 a      616 c      536 g      869 t
ORIGIN

Query Match      100.0%; Score 321; DB 9; Length 2838;
Best Local Similarity 100.0%; Pred. No. 5.1e-71;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGGAACCTGCGCTTTCTCATCATGTGTTTCCATATACATATGCTGTTCC 60
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DB 1892 GGTGGAACCTGCGCTTTCTCATCATGTGTTTCCATATACATATGCTGTTCC 1951

QY 61 ATTCAAAAACCGCCTTCGACAGCACAGAAAGTGAAGTGTGTTTGAAGAGAGTGCT 120
    |||||
DB 1952 ATTCAAAAACCGCCTTCGACAGCACAGAAAGTGAAGTGTGTTTGAAGAGAGTGCT 2011

QY 121 GTTGAATTCGTTTCTTTTATAGTGTCTCTGATGCCATCTGCTGATTCCTATATT 180
    |||||
DB 2012 GTTGAATTCGTTTCTTTTATAGTGTCTCTGATGCCATCTGCTGATTCCTATATT 2071

QY 181 GTAGTAAATACCTTCCCTCTTCGCGGTGAATAATACACACATACATCTCGGATA 240
    |||||
DB 2072 GTAGTAAATACCTTCCCTCTTCGCGGTGAATAATACACACATACATCTCGGATA 2131

QY 241 GTGATTTTTTCTTCGAGTTAACAGTCTTTGAATCCATCTCTATCTCACAACC 300
    |||||
DB 2132 GTGATTTTTTCTTCGAGTTAACAGTCTTTGAATCCATCTCTATCTCACAACC 2191

QY 301 AACTTTTAAAGACAAGTTG 321
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DB 2192 AACTTTTAAAGACAAGTTG 2212

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Db	2108	GTGCTTAAGATCCCTGTCTCTCTCTCTTCAAGTGGAGATACAGGACAGCAATCATCTCCCTGGATC	2167
QY	241	GTGATTTTTTTTCCTTCACAGTATGCTTTGAATCCATCTCTATACTCTCAACAAC	300
Db	2168	GGGGTTTTTTTTCCTCCGGTGAACAGCGCCTTAAACCCCATCTCTACACTCTGACGACC	2227
QY	301	AACTTTTTTAAAGACAAGTTG	321
Db	2228	TCCTTTTTTAAAGACAAGTTG	2248
RESULT 12			
LOCUS	AX147820/c	1018 bp	DNA
DEFINITION	Sequence 65 from Patent WO0136473.		linear
ACCESSION	AX147820		
VERSION	AX147820.1	GI:14346831	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1018) Vogel, G., Wood, L.S., Parodi, L.A., Hiesch, R.R., Lind, P., Silghom, J., Schellin, K.A., Kayles, P.S., Bannigan, C.M., Ruff, V., Sejlitz, T., and Huff, R.M.		
TITLE	Novel g protein-coupled receptors		
JOURNAL	Patent: WO 0136473-A 65 25-MAY-2001;		
FEATURES	PHARMACIA & UPJOHN COMPANY (US)		
Source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
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Best Local Similarity	100.0%; Pred. No. 2e-45;		
Matches 220; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	GGTGGAACCTGCGGGCTTTCTCATCTGAGTGGTTCTCTATATACATGTTCTGTCG	60
Db	539	GGTGGAACTGCGTGGCTTTCTCTCATCTGTTGTTCTTATATTACTATGTTCTGTTCC	480
QY	61	ATTCAAAAACCGCGCTTCAGACACACAGAAAGTAAGAAATGTTTGAAGAGAGGTGCT	120
Db	479	ATTCAAAAACCGCGCTTCAGACACACAGAAAGTAAGAAATGTTTGAAGAGAGGTGCT	420
QY	121	GTTGCAATCGTTCTTTTATATAGTGTCTCTATGCAATCGTGGATTCCTGATTT	180
Db	419	GTTGCAATCGTTCTTTTATATAGTGTCTCTATGCAATCGTGGATTCCTGATTT	360
QY	181	GTAGTAAATCGTTTCCCTCTCCCGGGTGAAGAAATACAG	220
Db	359	GTAGTAAATCGTTTCCCTCTCCCGGGTGAAGAAATACAG	320
RESULT 13			
LOCUS	AL138708	170522 bp	DNA
DEFINITION	Human DNA sequence from clone RP11-332E15 on chromosome 13 Contains STSs, GSSs and a CpG island, complete sequence.		
ACCESSION	AL138708		
VERSION	AL138708.17	GI:11337618	
KEYWORDS	HTG; CpG island.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 170522) Phillimore, B.		
TITLE	Direct Submission		

JOURNAL

Submitted (01-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk

Requests: clonerequests@sanger.ac.uk

On Nov 10, 2000 this sequence version replaced g1:1121365. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TRERBL; Wp., WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/Celegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/hrl3>

This sequence is the entire insert of clone RP11-432E15. The left end of clone RP11-154I23 is at 137612 in this sequence. The true right end of clone RP11-95N14 is at 13246 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-432E15 is from the library RPCT-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/dacpac/home.htm>

VECTOR: pBACE3.6.

location/Qualifiers

source

1. .170522

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="13"

/clone="RP11-432E15"

/clone\_id="RPCT-11.2"

19. .289

/note="match: GSS: Em:A0549338"

194. .299

/note="53 copies 2 mer tg 71% conserved"

208. .299

/note="23 copies 4 mer tgg 77% conserved"

1456. .1750

/note="AlusX repeat: matches 3. .300 of consensus"

2078. .2183

/note="MIR repeat: matches 6. .114 of consensus"

2600. .3122

/note="match: GSS: Em:A0529216"

2646. .2940

/note="AlusG repeat: matches 1. .302 of consensus"

3590. .3894

/note="AlusQ repeat: matches 1. .296 of consensus"

3926. .4462

/note="L2 repeat: matches 2233. .2750 of consensus"

4658. .4805

/note="L2 repeat: matches 2355. .2503 of consensus"

4911. .5224

/note="AlusG repeat: matches 1. .312 of consensus"

5237. .5332

/note="L2 repeat: matches 2575. .2694 of consensus"

5788. .6085

/note="AluJo repeat: matches 3. .301 of consensus"

7355. .7747

/note="sequence from overlapping clone BA15909 (AL136106). Assembly confirmed by restriction digest."

7388. 7487

/note="50 copies 2 mer at 63% conserved"

7396. .7487

/note="23 copies 4 mer at 66% conserved"

7884. .7915

/note="MER20 repeat: matches 30. .62 of consensus"

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repeat_region 8220..8376 /note="MER20 repeat: matches 62..210 of consensus"  
misc_feature 8975..8985 /note="sequence from overlapping clone  
bA15909(A136106).Assembly confirmed by restriction  
digest."  
repeat_region 9078..9121 /note="11 copies 4 mer ca 100% conserved"  
misc_feature complement(9603..10104)  
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11234..11331  
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(A136106).Assembly confirmed by restriction digest."  
complement(11953..12400)  
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12477..12601  
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12713..12980  
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/note="match: GSS: Em:AQ032630"  
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16061..16342  
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16343..16655  
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16656..16680  
/note="MER1B repeat: matches 244..305 of consensus"  
complement(17019..17275)  
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17087..17515  
/note="match: GSS: Em:AQ817416"  
17278..17794  
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18301..18381  
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20403..20559  
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20870..21069  
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20937..21076  
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21080..21392  
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21395..21538  
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23716..23960  
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23961..24213  
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24214..24342  
/note="L2 repeat: matches 2617..2747 of consensus"  
25636..25785  
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25638..25810  
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26013..26227  
/note="MIR repeat: matches 10..256 of consensus"
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repeat_region 28639..28960 /note="Alusq repeat: matches 1..310 of consensus"  
repeat_region 29689..29861 /note="L2 repeat: matches 2006..2186 of consensus"  
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29901..30075  
/note="MER5A repeat: matches 1..184 of consensus"  
complement(30119..30414)  
/note="match: GSS: Em:AQ230143"  
32462..32774  
/note="Alusx repeat: matches 1..312 of consensus"  
32807..32877  
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35365..35806  
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match: SFS: Em:G55301"  
complement(36043..36433)  
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36420..36469  
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36429..36961  
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36452..36845  
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39203..39242  
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39250..39648  
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39703..39750  
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39859..39976  
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/note="Aluy repeat: matches 39..310 of consensus"
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QY 1 GGTGTGAACCTGCTGCGTTTCTCATCTGTTTCTTCTATATTAATGTTCTGTC 60  
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QY 61 ATTCAAAAACCCGCTTGACACACAGAAAGTAATGTTTGGAGAAGAGTGCT 120  
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Db 42094 ATTCAAAAACCCGCTTGACACACAGAAAGTAATGTTTGGAGAAGAGTGCT 42153  
  
QY 121 GTTCAATGCTTCTTTTATAGTGTTCGTATGCAATCTCTGATTCCTGATTT 180  
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Db 42154 GTTCAATGCTTCTTTTATAGTGTTCGTATGCAATCTCTGATTCCTGATTT 42213  
  
QY 181 GTAGTAAATCTTTCCTTCCTCCGGGTGGAATACAG 220  
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Db 42214 GTAGTAAATCTTTCCTTCCTCCGGGTGGAATACAG 42253  
  
RESULT 14  
AX128507 1191 bp DNA linear PAT 15-MAY-2001  
LOCUS AX128507  
DEFINITION Sequence 15 from Patent WO0131014.  
ACCESSION AX128507  
VERSION AX128507.1 GI:14134974  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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PN WO200214496-A2.

Human G protein-coupled receptor 120	Human NGRP57 coding sequence	Human expressed protein	Human musculoskeletal system	Human cDNA SEQ ID	Human cDNA encoding for	Human endocrine protein	DNA encoding remaining	CDNA encoding novel	Human expressed protein	DNA encoding novel	Human expressed protein	DNA encoding novel	Human CON222 G protein-coupled receptor	Human GPCR protein	Human LGRT long form	Human LGRT short form	Human OREF ORF1250	Human HGR101 G-protein-coupled receptor	CDNA encoding Drosophila melanogaster	Drosophila melanogaster	CDNA encoding Drosophila melanogaster	Drosophila melanogaster	DNA encoding Drosophila melanogaster	Drosophila melanogaster	Drosophila melanogaster	Human immune system	Human immune system	Human immune system	Human secreted protein	Human prostate epithelial	Human immune/haematopoietic	Nucleotide sequence
--------------------------------------	------------------------------	-------------------------	------------------------------	-------------------	-------------------------	-------------------------	------------------------	---------------------	-------------------------	--------------------	-------------------------	--------------------	---	--------------------	----------------------	-----------------------	--------------------	---	---------------------------------------	-------------------------	---------------------------------------	-------------------------	--------------------------------------	-------------------------	-------------------------	---------------------	---------------------	---------------------	------------------------	---------------------------	-----------------------------	---------------------

PD	xx		21-FEB-2002.	
PF	xx		15-AUG-2001; 2001MO-US25513.	
PR	xx		15-AUG-2000; 2000US-225262P.	
PA	xx	(PHAA ) PHARMACIA & UPJOHN CO.		
PI	xx	Lind P;		
DR	xx	WPI; 2002-269192/31.		
P	xx	P-PSDB; AAE20148.		
PT	xx	An isolated nucleic acid molecule encoding novel G-protein coupled		
PT	xx	receptor polypeptide which is useful for treating obesity, diabetes,		
PT	xx	Parkinson's disease, manic depression, migraine, rheumatoid arthritis		
XX	xx	Claim 4; Page 60; 93pp; English.		
CC	cc	The patent discloses novel G-protein coupled receptor (ngPCR)-1079 genes		
CC	cc	and their corresponding proteins..Sequences of the invention are useful		
CC	cc	for treating diseases such as viral infections caused by human immuno-		
CC	cc	deficiency virus (HIV)-1 or 2, central nervous system (CNS) disorders		
CC	cc	(e.g. pain, including migraine, stroke, manic depression), metabolic		
CC	cc	disorders (e.g. Obesity and anorexia), cancers, cardiovascular disorders		
CC	cc	(e.g. Type 2 diabetes, myocardial infarction, hypertension), degenerative		
CC	cc	disorders (e.g. Parkinson's disease, Alzheimer's disease), neurological		
CC	cc	rheumatoid arthritis, thyroid disorders, autoimmune disorders, hormonal		
CC	cc	disorders, renal failure, psoriasis and movement disorders. The present		
SQ	xx	sequence is a DNA encoding human ngPCR-1079 protein:		
		Sequence 321 BP; 76 A; 67 C; 59 G; 119 T; 0 other;		
		Query Match 100.0%; Score 321; DB 24; Length 321;		
		Best Local Similarity 100.0%; Pred. No. 1.2e-86;		
		Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1	GGTGTAACCTTCGGCTTTCATCATATGTTTCTATATTACTATAGTTCTGTTCC	60	
Db	1	GGTGTAACCTTCGGCTTTCATCATATGTTTCTATATTACTATAGTTCTGTTCC	60	
OY	61	ATTCAAAAACCGCGCTTGACACACCACAGAAGTAGAATGTTTTGGAAGAAGTGCGT	120	
Db	61	ATTCAAAAACCGCGCTTGACACACCACAGAAGTAGAATGTTTTGGAAGAAGTGCGT	120	
OY	121	GTCGAATTCGTTTCTTTTATAGTGTCTGTGANGCATGTGCATGTTCTGTATTT	180	
Db	121	GTCGAATTCGTTTCTTTTATAGTGTCTGTGANGCATGTGCATGTTCTGTATTT	180	
OY	181	GTAGTTAAAAATCCTTCCCTCTTCGCGGGTGAATAACACACAATGACTTCGGATA	240	
Db	181	GTAGTTAAAAATCCTTCCCTCTTCGCGGGTGAATAACACACAATGACTTCGGATA	240	
OY	241	GGATTTTTTTCCTTCACAGTAAAGTGGTTGAAATCCAATCTATATCTCACAAAC	300	
Db	241	GGATTTTTTTCCTTCACAGTAAAGTGGTTGAAATCCAATCTATATCTCACAAAC	300	
OY	301	AACTTTTTAAGGACAAAGTTG 321		
Db	301	AACTTTTTAAGGACAAAGTTG 321		
RESULT 2				
ABLA0194		standard; cDNA; 1065 BP.		
AC		ABLA0194;		
DT		23-MAY-2002 (first entry)		

XX	Human G-protein-coupled receptor TGR17-4 encoding cDNA SEQ ID NO.11.
KW	Human; G-protein-coupled receptor; TGR17-4; nootropic; antiinflammatory;
KW	vasotrophic; immunomodulatory; cyostatic; gene therapy; protein therapy;
KW	neurological; inflammatory; circulatory; degenerative; immune system;
KW	digestive disease; cancer; gene; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	CDS
FT	1..1065
FT	/*tag=
FT	/partial a
FT	/product= "TGR17-4"
FT	/note= "no stop codon given"
XX	
PN	MO200204640-A1.
XX	
PD	17-JAN-2002.
XX	
PF	06-JUL-2001; 2001WO-JP05878.
XX	
PR	07-JUL-2000; 2000JP-0211989.
PR	18-DEC-2000; 2000JP-0383794.
XX	
PA	(TAKE ) TAKEDA CHEM IND LTD.
XX	
PI	Moriya T, Ito T, Shintani Y, Miyajima N;
XX	
DR	WPI: 2002-179706/23.
XX	
DR	P-PSDB; ABB06253.
XX	
PT	G-protein coupled receptor protein TGR17 of human origin and DNA
PT	encoding it for diagnosis and treatment of cancer and circulatory and
PT	other diseases associated with its expression -
XX	
XX	Claim 7; Page 125-126; 145pp; Japanese.
XX	
XX	The present invention describes a human guanine nucleotide binding
CC	protein (G-protein) coupled receptor protein designated TGR17, which has
CC	5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having
CC	additional residues at the N-terminal. The TGR17 proteins have nootropic,
CC	antiinflammatory, vasotropic, immunomodulator and cyostatic activities.
CC	The TGR17 polynucleotides and protein can be used in gene therapy and
CC	protein therapy. G-protein coupled receptor proteins are cell membrane
CC	proteins mediating the cellular response to a large variety of signalling
CC	molecules. The TGR17 polynucleotides and proteins can be used in the
CC	diagnosis, treatment and prevention of diseases including neurological,
CC	inflammatory, circulatory, degenerative, immune system and digestive
CC	diseases and cancer. The present sequence encodes human TGR17-4 from the
CC	present invention.
XX	
XX	Sequence 1065 BP; 277 A; 214 C; 213 G; 361 T; 0 other;
XX	
XX	Query Match 100.0%; Score 321; DB 24; Length 1065;
XX	Best Local Similarity 100.0%; Pred. No. 1.9e-86;
XX	Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GGTGTGACCTGGCTGGCTTTCTCATCATTTGTTTCTATATTAGTATGTCGTGCC 60
DB	GGTGTGACCTGGCTGGCTTTCTCATCATTTGTTTCTATATTAGTATGTCGTGCC 648
QY	61 ATTCAAAAAACCCGCTTGGACACACAGAAAGTAAATGTTTGGAAAGAGGTGGCT 120
DB	ATTCAAAAAACCCGCTTGGACACACAGAAAGTAAATGTTTGGAAAGAGGTGGCT 708
QY	121 GTTGTCAATGTTTCTTTTATAGTCTCGATGATCGCATTTGCTGATTCCTGTATT 180
DB	GTTGTCAATGTTTCTTTTATAGTCTCGATGATCGCATTTGCTGATTCCTGTATT 768
QY	181 GTAGTAAATCTTCTTCCCTCTTCGCGGTGAATACAGACACATGACTTCGTGATA 240
DB	GTAGTAAATCTTCTTCCCTCTTCGCGGTGAATACAGACACATGACTTCGTGATA 828

QY 241 GTGATTTTTCCTTCAGTTACAGTGTGTAATCCATCCCTATACCTCACAACC 300  
 |||||||  
 DB 829 GTGATTTTTCCTTCAGTTACAGTGTGTAATCCATCCCTATACCTCACAACC 888  
 |||||||  
 QY 301 AACCTTTTAAAGACAACTTG 321  
 |||||||  
 DB 889 AACCTTTTAAAGACAACTTG 909  
 |||||||

RESULT 3  
 AAS07943  
 ID AAS07943 standard; cDNA: 1068 BP.  
 XX  
 AC AAS07943:  
 XX  
 DT 23-OCT-2001 (first entry)  
 XX  
 DE Human cDNA encoding G-protein coupled receptor, hRUP16.  
 XX  
 KW Human; G-protein coupled receptor; GPCR; hRUP16; agonist:  
 KM inverse agonist; lung cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1068  
 FT /\*tag= a  
 FT /product= "hRUP16"  
 XX  
 PN WO200136471-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PE 16-NOV-2000; 2000MO-US11509.  
 XX  
 PR 17-NOV-1999; 99US-0166088.  
 PR 17-NOV-1999; 99US-0166099.  
 PR 17-NOV-1999; 99US-0166369.  
 PR 23-DEC-1999; 99US-0171900.  
 PR 23-DEC-1999; 99US-0171901.  
 PR 23-DEC-1999; 99US-0171902.  
 PR 11-FEB-2000; 2000US-0181749.  
 PR 14-MAR-2000; 2000US-0189258.  
 PR 14-MAR-2000; 2000US-0189259.  
 PR 10-APR-2000; 2000US-0195898.  
 PR 10-APR-2000; 2000US-0195899.  
 PR 10-APR-2000; 2000US-0196078.  
 PR 28-APR-2000; 2000US-0200419.  
 PR 12-MAY-2000; 2000US-0203630.  
 PR 12-MAY-2000; 2000US-0210741.  
 PR 12-JUN-2000; 2000US-0210982.  
 PR 21-AUG-2000; 2000US-0226760.  
 PR 26-SEP-2000; 2000US-0235418.  
 PR 26-SEP-2000; 2000US-0235779.  
 PR 20-OCT-2000; 2000US-0242332.  
 PR 20-OCT-2000; 2000US-0242343.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 XX  
 PI Chen R, Dang HT, Lowitz KP;  
 XX  
 DR WPI: 2001-355616/37.  
 DR P-PSDB; AAU04370.  
 XX  
 PT Endogenous and non-endogenous versions of human G-protein coupled  
 PT receptors for direct identification of candidate compounds as agonists,  
 PT inverse agonists or partial agonists for use as therapeutic agents -  
 XX  
 PS Claim 35; Page 104-105, 159pp; English.  
 XX  
 CC The sequence encodes a human G-protein coupled receptor (GPCR),  
 CC hRUP16 the endogenous and non-endogenous, constitutively activated

CC versions of human G-protein coupled receptors (GPCR), are useful for  
 CC direct identification of candidate compounds as receptor agonists,  
 CC inverse agonists or partial agonists having applicability as therapeutic  
 CC agents for treating diseases related to GPCR, e.g. lung cancer.  
 CC Non-endogenous version of human GPCRs are also utilized in research  
 CC settings and in vitro and in vivo system, incorporating GPCRs can be  
 CC utilized to elucidate and understand the roles these receptors  
 CC play in the human condition, both normal and diseased.  
 XX  
 SQ Sequence 1068 BP; 278 A; 215 C; 214 G; 361 T; 0 other;  
 Query Match 100.0%; Score 321; DB 22; Length 1068;  
 Best Local Similarity 100.0%; Pred. No. 1,9e-86;  
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGTGTGAACCTGCTGGCTTTCTCATCATCTGTTTCCATATATAGTCTGTGTC 60  
 |||||||  
 DB 589 GGTGTGAACCTGCTGGCTTTCTCATCATCTGTTTCCATATATAGTCTGTGTC 648  
 |||||||  
 QY 61 ATTCAAAAACCGCCTTCAGACCCAGAGATGAAGAAATGTTTGAAGAGAGTGCT 120  
 |||||||  
 DB 649 ATTCAAAAACCGCCTTCAGACCCAGAGATGAAGAAATGTTTGAAGAGAGTGCT 708  
 |||||||  
 QY 121 GTTGCAATCGTTCTTTTATATAGTCTCTGTGATGCCATCTGCGATTCTGTATT 180  
 |||||||  
 DB 709 GTTGCAATCGTTCTTTTATATAGTCTCTGTGATGCCATCTGCGATTCTGTATT 768  
 |||||||  
 QY 181 GTAGTTAAATCTTTCCCTCTCCGGGTGAATAATACAGACAAATGCTCTGATA 240  
 |||||||  
 DB 769 GTAGTTAAATCTTTCCCTCTCCGGGTGAATAATACAGACAAATGCTCTGATA 828  
 |||||||  
 QY 241 GTGATTTTTCCTTCAGTTACAGTGTGTAATCCATCCCTATACCTCACAACC 300  
 |||||||  
 DB 829 GTGATTTTTCCTTCAGTTACAGTGTGTAATCCATCCCTATACCTCACAACC 888  
 |||||||  
 QY 301 AACCTTTTAAAGACAACTTG 321  
 |||||||  
 DB 889 AACCTTTTAAAGACAACTTG 909  
 |||||||

RESULT 4  
 ABL40192  
 ID ABL40192 standard; cDNA: 1473 BP.  
 XX  
 AC ABL40192:  
 XX  
 DT 23-MAY-2002 (first entry)  
 XX  
 DE Human G protein-coupled receptor TGR17-3 encoding cDNA SEQ ID NO:8.  
 XX  
 KW Human; G protein-coupled receptor; TGR17-3; neotropic; antiinflammatory;  
 KW vasotropic; immunomodulator; cyostatic; gene therapy; protein therapy;  
 KW neurological; inflammatory; circulatory; degenerative; immune system;  
 KW digestive disease; cancer; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1473  
 FT /\*tag= a  
 FT /partial  
 FT /product= "TGR17-3"  
 FT /note= "no stop codon given"  
 XX  
 PN WO200204640-A1.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 06-JUL-2001; 2001WO-JP05878.  
 XX  
 PR 07-JUL-2000; 2000JP-0211989.  
 PR 18-DEC-2000; 2000JP-0383794.  
 XX



Db 1369 AACCTTTTAAAGACAAGTTG 1389

RESULT 6

ABL40188

ID ABL40188 standard; cDNA; 1830 BP.

XX ABL40188;

XX 23-MAY-2002 (first entry)

DE Human G protein-coupled receptor TGR17-1 encoding cDNA SEQ ID NO:2.

XX Human; G protein-coupled receptor; TGR17-1; nootropic; antiinflammatory;

KW vasotropic; immunomodulator; cytostatic; gene therapy; protein therapy;

KW neurological; inflammatory; circulatory; degenerative; immune system;

KW digestive disease; cancer; gene; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH 1.1830

FT /tag- a

FT /partial

FT /product= "TGR17-1"

FT /note= "no stop codon given"

XX

XX WO200204640-A1.

XX

XX 17-JAN-2002.

XX

XX 06-JUL-2001; 2001WO-JP05878.

XX

XX 07-JUL-2000; 2000JP-0211989.

PR 18-DEC-2000; 2000JP-0383794.

XX

PA (TAKE ) TAKEDA CHEM IND LTD.

XX

PI Moriya T, Ito T, Shintani Y, Miyajima N;

XX

XX WPI: 2002-179706/23.

DR P-PSDB: ABB06250.

XX

PT G-protein coupled receptor protein TGR17 of human origin and DNA

PT encoding it for diagnosis and treatment of cancer and circulatory and

PT other diseases associated with its expression

XX

XX Claim 7; Page 114-115; 145pp; Japanese.

XX

XX The present invention describes a human guanine nucleotide binding

CC protein (G protein) coupled receptor protein designated TGR17, which has

CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having

CC additional residues at the N-terminal. The TGR17 proteins have nootropic,

CC antiinflammatory, vasotropic, immunomodulator and cytostatic activities.

CC The TGR17 polynucleotides and protein can be used in gene therapy and

CC protein therapy. G-protein coupled receptor proteins are cell membrane

CC proteins mediating the cellular response to a large variety of signalling

CC molecules. The TGR17 polynucleotides and proteins can be used in the

CC diagnosis, treatment and prevention of diseases including neurological,

CC inflammatory, circulatory, degenerative, immune system and digestive

CC diseases and cancer. The present sequence encodes human TGR17-1 from the

CC present invention.

XX

XX Sequence 1830 BP; 516 A; 377 C; 351 G; 586 T; 0 other:

SO

Query Match 100.0%; Score 321; DB 24; Length 1830;

Best Local Similarity 100.0%; Pred. No. 2.2e-86;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTCGAACTGCTGCTTCTCTCATGTCGTTCTTCTCATATGATGTCGTC 60

DB 1354 GGTCGAACTGCTGCTTCTCTCATGTCGTTCTTCTCATATGATGTCGTC 1413

OY 61 ATTCAAAAACCGCCTTGACAGACAGAAATGTTTGGAGAGAGGTGGCT 120

DB 1414 ATTCAAAAACCGCCTTGACAGACAGAAATGTTTGGAGAGAGGTGGCT 1473

OY 121 GTTGCAAAATCGTTTCTTTTATAGTGTCTCTGATGCAATGCTGATTCCTGATTT 180

DB 1474 GTTGCAAAATCGTTTCTTTTATAGTGTCTCTGATGCAATGCTGATTCCTGATTT 1533

OY 181 GTAGTTAAATCTTTCCTCTCCGGGTGGAAATACACAGACAAATGACTTCCTGGATA 240

DB 1534 GTAGTTAAATCTTTCCTCTCCGGGTGGAAATACACAGACAAATGACTTCCTGGATA 1593

OY 241 GGTATTTTCTCTCCAGTTTACAGTGTCTGAAATCCATCTCTATCTCTCAAC 300

DB 1594 GGTATTTTCTCTCCAGTTTACAGTGTCTGAAATCCATCTCTATCTCTCAAC 1653

OY 301 AACCTTTTAAAGACAAGTTG 321

DB 1654 AACCTTTTAAAGACAAGTTG 1674

RESULT 7

ABK51947

ID ABK51947 standard; cDNA; 2142 BP.

XX ABK51947;

XX 27-AUG-2002 (first entry)

XX

XX cDNA encoding human G-protein coupled receptor HGPBMY5 splice variant.

XX

XX Human; G-protein coupled receptor; GPCR; HGPBMY5; colon; brain;

KW neurological disorder; infection; human immunodeficiency virus; HIV;

KW anti-allergic; antiasthmatic; dermatological; antiarteriosclerotic;

KW antidiabetic; nephrotoxic; osteopathic; antiarthritic;

KW antiinflammatory; antineumatic; antithyroid; cytostatic; vulnery;

KW virucide; antibacterial; antifungal; antiparasitic; protozoicide;

KW antihelminthic; nootropic; neuroprotective; antidepressant;

KW anticonvulsant; antiparkinsonian; neuroleptic; anti-HIV; gene; ss.

XX

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH 1.2142

FT /tag- a

FT /product= "GPCR HGPBMY5"

XX

XX WO200226824-A2.

XX

XX 04-APR-2002.

XX

XX 26-SEP-2001; 2001WO-US30365.

XX

XX 27-SEP-2000; 2000US-235713P.

PR 16-JAN-2001; 2001US-261781P.

PR 19-JUL-2001; 2001US-306605P.

PR 03-AUG-2001; 2001US-310436P.

XX

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

PA Feder JN, Muntler G, Ramanathan CS, Hawken DR;

XX

XX WPI: 2002-435196/46.

DR P-PSDB: AA097159.

XX

XX Novel G protein-coupled receptor, HGPBMY5 polypeptide, useful for

PT treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative

PT colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,

PT osteoarthritis

XX

XX Claim 1; Fig 5; 148pp; English.

CC The present invention relates to the isolation of a novel human  
CC G-protein coupled receptor (GPCR) (HGRBM5), and the polynucleotide  
CC sequence encoding it. The HGRBM5 polypeptide and polynucleotide  
CC are useful for preventing, treating or ameliorating a disease,  
CC disorder or condition related to the colon, brain, ovaries, thymus,  
CC lungs or immune system. They are particularly useful for the  
CC treatment or prevention of cancers, immune disorders, neurological  
CC disorders, and diseases related to the brain, ovaries, thymus or  
CC lungs. The polynucleotide sequence is useful for diagnosing or  
CC determining susceptibility to infections such as bacterial, fungal,  
CC protozoan and viral infections, particularly infections caused by  
CC human immunodeficiency virus (HIV or HIV-2). The present sequence  
CC encodes a splice variant of human GPCR HGRBM5.

CC Sequence 2142 BP; 613 A; 435 C; 408 G; 686 T; 0 other;

Query Match 100.0%; Score 321; DB 24; Length 2142;  
Best Local Similarity 100.0%; Pred. NO. 2.4e-86;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTGGAACCTGCTGCTTTCTCATCTGTTTCTTTCATATTTACTATGTCGTTCC 60  
DB 1663 GGCTGGAACCTGCTGCTTTCTCATCTGTTTCTTTCATATTTACTATGTCGTTCC 1722  
QY 61 ATTCAAAAACCGCTTGCAGACACAGAGTAAGTAATTTTGGAGAGAGTGCT 120  
DB 1723 ATTCAAAAACCGCTTGCAGACACAGAGTAAGTAATTTTGGAGAGAGTGCT 1782  
QY 121 GTTGCAATCGTTCTTTTATAGTGTCTGTATGTCATCTGTCGATCTGTAATTT 180  
DB 1783 GTTGCAATCGTTCTTTTATAGTGTCTGTATGTCATCTGTCGATCTGTAATTT 1842  
QY 181 GTAGTAAATCCTTCCCTTCCCTGCTGGAATPACACAGACAAATGCTTCTGATA 240  
DB 1843 GTAGTAAATCCTTCCCTTCCCTGCTGGAATPACACAGACAAATGCTTCTGATA 1902  
QY 241 GTGATTTTTTCTTCCAGTAAACAGTGTGTAATCAATCCCTATCTGACAAAC 300  
DB 1903 GTGATTTTTTCTTCCAGTAAACAGTGTGTAATCAATCCCTATCTGACAAAC 1962  
QY 301 AACTTTTTTAAGACAAAGTTG 321  
DB 1963 AACTTTTTTAAGACAAAGTTG 1983

## RESULT 8

ABLA0197 standard; cDNA; 2190 BP.

ABLA0197;

23-MAY-2002 (first entry)

Human G protein-coupled receptor TGR17-6 encoding cDNA SEQ ID NO:16.

Human: G protein-coupled receptor; TGR17-6; neotropic; antiinflammatory;  
neurological; immunomodulator; cytostatic; gene therapy; protein therapy;  
neurological; inflammatory; circulatory; degenerative; immune system;  
digestive disease; cancer; gene; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 1..2190

FT /\*tag= a

FT /partial= "TGR17-6"

FT /note= "no stop codon given"

W0200204640-A1.

17-JAN-2002.

XX

PF 06-JUL-2001; 2001WO-JP05878.

XX 07-JUL-2000; 2000JP-0211989.

PR 18-DEC-2000; 2000JP-0383794.

XX (TAKE ) TAKEDA CHEM IND LTD.

PI Moriya T, Ito T, Shintani Y, MiyaJima N;

XX WPI: 2002-179706/23.

DR P-PSDB: ABB06255.

XX

PT G-protein coupled receptor protein TGR17 of human origin and DNA

PT encoding it for diagnosis and treatment of cancer and circulatory and

PT other diseases associated with its expression -

XX

PS Claim 7; Page 135-136; 145pp; Japanese.

XX

CC The present invention describes a human guanine nucleotide binding

CC protein (G protein), coupled receptor protein designated TGR17, which has

CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having

CC additional residues at the N-terminal. The TGR17 proteins have neotropic,

CC antiinflammatory, vasotropic, immunomodulator and cytostatic activities.

CC The TGR17 polynucleotides and protein can be used in gene therapy and

CC protein therapy. G-protein coupled receptor proteins are cell membrane

CC proteins mediating the cellular response to a large variety of signalling

CC molecules. The TGR17 polynucleotides and proteins can be used in the

CC diagnosis, treatment and prevention of diseases including neurological,

CC inflammatory, circulatory, degenerative, immune system and digestive

CC diseases and cancer. The present sequence encodes human TGR17-6 from the

CC present invention.

XX

SQ Sequence 2190 BP; 626 A; 457 C; 409 G; 698 T; 0 other;

Query Match 100.0%; Score 321; DB 24; Length 2190;  
Best Local Similarity 100.0%; Pred. No. 2.4e-86;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTGGAACCTGCTGCTTTCTCATCTGTTTCTTTCATATTTACTATGTCGTTCC 60

DB 1714 GGCTGGAACCTGCTGCTTTCTCATCTGTTTCTTTCATATTTACTATGTCGTTCC 1773

QY 61 ATTCAAAAACCGCTTGCAGACACAGAGTAAGTAATTTTGGAGAGAGTGCT 120

DB 1774 ATTCAAAAACCGCTTGCAGACACAGAGTAAGTAATTTTGGAGAGAGTGCT 1833

QY 121 GTTGCAATCGTTCTTTTATAGTGTCTGTATGTCATCTGTCGATCTGTAATTT 180

DB 1834 GTTGCAATCGTTCTTTTATAGTGTCTGTATGTCATCTGTCGATCTGTAATTT 1893

QY 181 GTAGTAAATCCTTCCCTTCCCTGCTGGAATPACACAGACAAATGCTTCTGATA 240

DB 1894 GTAGTAAATCCTTCCCTTCCCTGCTGGAATPACACAGACAAATGCTTCTGATA 1953

QY 241 GTGATTTTTTCTTCCAGTAAACAGTGTGTAATCAATCCCTATCTGACAAAC 300

DB 1954 GTGATTTTTTCTTCCAGTAAACAGTGTGTAATCAATCCCTATCTGACAAAC 2013

QY 301 AACTTTTTTAAGACAAAGTTG 321

DB 2014 AACTTTTTTAAGACAAAGTTG 2034

RESULT 9

ABK51944 standard; cDNA; 2214 BP.

ABK51944;

27-AUG-2002 (first entry)

cdna encoding human G-protein coupled receptor HGRBM5.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

KM Human; G-protein coupled receptor; GPCR; HGPBRM5; colon; brain;  
 KM ovary; thymus; lung; immune system; cancer; immune disorder;  
 KM neurological disorder; infection; human immunodeficiency virus; HIV;  
 KM antiallergic; antisthmatic; dermatological; antiarteriosclerotic;  
 KM antitumor; antidiabetic; nephrotropic; osteopathic; antiarthritic;  
 KM antiinflammatory; antineumatic; antihypoid; cytosolic; vulnary;  
 KM virucide; antibacterial; antifungal; antiparasitic; protozoacide;  
 KM antihelminthic; nootropic; neuroprotective; antidepressant;  
 KM anticonvulsant; antiparkinsonian; neuroleptic; anti-HIV; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2214  
 FT /\*tag= a  
 FT /product= "GPCR HGPBRM5"  
 XX  
 PN W0200226824-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 26-SEP-2001; 2001MO-US30365.  
 XX  
 PR 27-SEP-2000; 2000US-235713P.  
 PR 16-JAN-2001; 2001US-261781P.  
 PR 19-JUL-2001; 2001US-30605P.  
 PR 03-AUG-2001; 2001US-310436P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Feder JN, Mintier G, Ramanathan CS, Hawken DR;  
 XX  
 DR WPI; 2002-435196/46.  
 XX  
 PT P-PSDB; AA097158.  
 XX  
 PT Novel G protein-coupled receptor, HGPBRM5 polypeptide, useful for  
 PT treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative  
 PT colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,  
 PT osteoarthritis  
 XX  
 PS Claim 1; Fig 1; 148pp; English.  
 XX  
 CC The present invention relates to the isolation of a novel human  
 CC G-protein coupled receptor (GPCR) (HGPBRM5), and the polynucleotide  
 CC sequence encoding it. The HGPBRM5 polypeptide and polynucleotide  
 CC are useful for preventing, treating or ameliorating a disease,  
 CC disorder or condition related to the colon, brain, ovaries, thymus,  
 CC lungs or immune system. They are particularly useful for the  
 CC treatment or prevention of cancers, immune disorders, neurological  
 CC disorders, and diseases related to the brain, ovaries, thymus or  
 CC lungs. The polynucleotide sequence is useful for diagnosing or  
 CC determining susceptibility to infections such as bacterial, fungal,  
 CC protozoan and viral infections, particularly infections caused by  
 CC human immunodeficiency virus (HIV or HIV-2). The present sequence  
 CC encodes human GPCR HGPBRM5.  
 CC  
 XX  
 SQ Sequence 2214 BP; 638 A; 457 C; 416 G; 703 T; 0 other;  
 XX  
 Query Match 100.0%; Score 321; DB 24; Length 2214;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-86;  
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 GGTTGAACTGCTGGCTTTTCATCATGTTGTTTCATATATACATGTCGTTCC 60  
 Db 1735 GGTTGAACTGCTGGCTTTTCATCATGTTGTTTCATATATACATGTTCC 1794  
 QY 61 ATTCAAAAACCGCCTTGACAGACACAGAGTAAGAAATGTTTGGAGAGAGTGCT 120  
 Db 1795 ATTCAAAAACCGCCTTGACAGACACAGAGTAAGAAATGTTTGGAGAGAGTGCT 1854  
 QY 121 GTTCAAAATGTTTCTTTTATATAGTGTCTCTATGTCATCTCTGATTTCCGTATTT 180  
 Db 1855 GTTCAAAATGTTTCTTTTATATAGTGTCTCTATGTCATCTCTGATTTCCGTATTT 1914

QY 181 GTAGTAAATCCCTTCCTCCGGGTGAATACAGACACAAATGACTTCGAGATA 240  
 Db 1915 GTAGTAAATCCCTTCCTCCGGGTGAATACAGACACAAATGACTTCGAGATA 1974  
 QY 241 GTGATTTTTCCTTCAGTTAAGAGTGCCTTGAATCCATCCTATACTGCACAACC 300  
 Db 1975 GTGATTTTTCCTTCAGTTAAGAGTGCCTTGAATCCATCCTATACTGCACAACC 2034  
 QY 301 AACTTTTAAAGACAACTTG 321  
 Db 2035 AACTTTTAAAGACAACTTG 2055  
 RESULT 10  
 ABL40196  
 ID ABL40196 standard; cDNA; 2262 BP.  
 XX  
 AC ABL40196;  
 XX  
 DT 23-MAY-2002 (first entry)  
 XX  
 DE Human G protein-coupled receptor TGR17-5 encoding cDNA SEQ ID NO:14.  
 XX  
 KM Human; G protein-coupled receptor; TGR17-5; nootropic; antiinflammatory;  
 KM vasotropic; immunomodulator; cytosolic; gene therapy; protein therapy;  
 KM neurological; inflammatory; circulatory; degenerative; immune system;  
 KM digestive disease; cancer; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2262  
 FT /\*tag= a  
 FT /partial  
 FT /product= "TGR17-5"  
 FT /note= "no stop codon given"  
 XX  
 PN W0200204640-A1.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 06-JUL-2001; 2001MO-JP05878.  
 XX  
 PR 07-JUL-2000; 2000JP-0211989.  
 PR 18-DEC-2000; 2000JP-0383794.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Moriya T, Ito T, Shintani Y, Miyajima N;  
 XX  
 DR WPI; 2002-179706/23.  
 DR P-PSDB; ABB06254.  
 XX  
 PT G-protein coupled receptor protein TGR17 of human origin and DNA  
 PT encoding it for diagnosis and treatment of cancer and circulatory and  
 PT other diseases associated with its expression  
 XX  
 PS Claim 7; Page 130-131; 145pp; Japanese.  
 XX  
 CC The present invention describes a human guanine nucleotide binding  
 CC protein (G protein) coupled receptor protein designated TGR17, which has  
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
 CC additional residues at the N-terminal. The TGR17 proteins have nootropic,  
 CC antiinflammatory, vasotropic, immunomodulator and cytosolic activities.  
 CC The TGR17 polynucleotides and protein can be used in gene therapy and  
 CC protein therapy. G-protein coupled receptor proteins are cell membrane  
 CC proteins mediating the cellular response to a large variety of signalling  
 CC molecules. The TGR17 polynucleotides and proteins can be used in the  
 CC diagnosis, treatment and prevention of diseases including neurological,  
 CC inflammatory, circulatory, degenerative, immune system and digestive  
 CC diseases and cancer. The present sequence encodes human TGR17-5 from the  
 CC present invention.

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XX  SQ      Sequence 2262 BP; 650 A; 467 C; 421 G; 724 T; 0 other;
Query Match          100.0%; Score 321; DB 24; Length 2262;
Best Local Similarity 100.0%; Pred. No. 2,4e-86;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGTGTGAACCTGGCTGCTTTCTCATCATGTTGTCTTCCATATATATGTTCTGTTCC 60
    |||||||
DB  1786 GGTGTGAACCTGGCTGCTTTCTCATCATGTTGTCTTCCATATATATGTTCTGTTCC 1845

QY  61 ATTCAAAAAACCCGCTTGCAGACCACAGAAAGTAAGCAATGTTTGGAGAAGAGTGCGCT 120
    |||||||
DB  1846 ATTCAAAAAACCCGCTTGCAGACCACAGAAAGTAAGCAATGTTTGGAGAAGAGTGCGCT 1905

QY  121 GTTGCAAAATCGTTCTTTTATAGTGTCTCATGATGTCATGCTGATGTTCTGATTT 180
    |||||||
DB  1906 GTTGCAAAATCGTTCTTTTATAGTGTCTCATGATGTCATGCTGATGTTCTGATTT 1965

QY  181 GTAGTTAAATCCTTTCCTCTCCGCGGTGAAATATACACACAATGACTTCTGTGATA 240
    |||||||
DB  1966 GTAGTTAAATCCTTTCCTCTCCGCGGTGAAATATACACACAATGACTTCTGTGATA 2025

QY  241 GTATTTTTCCTTCAGTTAAAGTGTGTAATGCAATCCTCTATCTTCACACACC 300
    |||||||
DB  2026 GTATTTTTCCTTCAGTTAAAGTGTGTAATGCAATCCTCTATCTTCACACACC 2085

QY  301 AACTTTTTTAAAGACAAGTGTG 321
    |||||||
DB  2086 AACTTTTTTAAAGACAAGTGTG 2106

RESULT 11
AAH51001/c
ID  AAH51001 standard; DNA; 1018 BP.
XX
AC  AAH51001;
XX
DT  28-AUG-2001 (first entry)
XX
DE  Human nGPCR57 coding sequence.
XX
KW  G protein-coupled receptor; nGPCR; seven transmembrane receptor;
    signal transduction; schizophrenia; thyroid disorder; renal failure;
    rheumatoid arthritis; CNS disorder; infection; metabolic disease;
    cardiovascular disease; proliferative disorder; hormonal disorder;
    neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
    attention deficit-hyperactivity disorder/attention deficit disorder;
    Parkinson's disease; migraine; senile dementia; inflammatory disease;
    rheumatoid arthritis; autoimmune disorder; respiratory ailment;
    neuroprotective; ds.
XX
OS  Homo sapiens.
XX
PN  WO200136473-A2.
XX
PD  25-MAY-2001.
XX
PF  16-NOV-2000; 2000MO-US31581.
XX
PR  16-NOV-1999; 99US-0165838.
    17-NOV-1999; 99US-0166071.
    19-NOV-1999; 99US-0166678.
    28-DEC-1999; 99US-0173396.
    22-FEB-2000; 2000US-0184129.
    28-FEB-2000; 2000US-0185421.
    28-FEB-2000; 2000US-0185554.
    02-MAR-2000; 2000US-0186530.
    03-MAR-2000; 2000US-0186811.
    09-MAR-2000; 2000US-0188114.
    17-MAR-2000; 2000US-0190310.
    21-MAR-2000; 2000US-0190800.
    20-APR-2000; 2000US-0198568.

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PR  02-MAY-2000; 2000US-0201190.
PR  08-MAY-2000; 2000US-0203111.
PR  25-MAY-2000; 2000US-0207094.
XX
PA  (PHAA ) PHARMACIA & UPJOHN CO.
PI  Vogell G, Wood LS, Parodi LA, Hlebsch RR, Lind P, Slightom J,
    Schellin KA, Kayes PS, Bannigan CM, Ruff V, Sejltz T, Huff RM;
    MPI: 2001-389826/41.
    P-PSDB; AAC80961.
PT  New G protein-coupled receptor (nGPCR-x) and its encoding
    polynucleotide useful for diagnosing and treating e.g. schizophrenia -
    Claim 4; Page 86; 261pp; English.
XX
PS  The present invention relates to novel G protein-coupled receptors
    (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
    28, 31-38, 40, 41, 53-60) and their coding sequences. The present
    sequence is the coding sequence for one such G protein-coupled receptor.
    GPCRs are also known as seven transmembrane receptors and function in
    signal transduction. The nGPCR coding sequences are useful for
    screening a human to diagnose a disorder affecting the brain or a
    predisposition, specifically schizophrenia. nGPCR are useful for
    identifying compounds useful for treating schizophrenia. Detection of
    nGPCR in a sample is useful as a diagnostic tool for diseases or
    disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,
    CNS disorders, infections such as HIV-1, metabolic and cardiovascular
    diseases, proliferative disorders and hormonal disorders. Modulators of
    nGPCR activity have the utility for treating neurological disorders,
    including schizophrenia, ADHD/ADD (attention deficit-hyperactivity
    disorder/attention deficit disorder), and neuronal disorders such as
    Alzheimer's disease, Parkinson's disease, migraine and senile dementia.
    CC Additional disorders include inflammatory conditions (e.g. Crohn's
    disease), rheumatoid arthritis, autoimmune disorders, cancers,
    CC respiratory ailments such as asthma, and inflammatory diseases e.g.
    CC inflammatory bowel disease.
XX
SQ  Sequence 1018 BP; 332 A; 179 C; 189 G; 318 T; 0 other;
Query Match          68.5%; Score 220; DB 22; Length 1018;
Best Local Similarity 100.0%; Pred. No. 4,1e-56;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGTGTGAACCTGGCTGCTTTCTCATCATGTTGTCTTCCATATATATGTTCTGTTCC 60
    |||||||
DB  539 GGTGTGAACCTGGCTGCTTTCTCATCATGTTGTCTTCCATATATATGTTCTGTTCC 480

QY  61 ATTCAAAAAACCCGCTTGCAGACCACAGAAAGTAAGCAATGTTTGGAGAAGAGTGCGCT 120
    |||||||
DB  479 ATTCAAAAAACCCGCTTGCAGACCACAGAAAGTAAGCAATGTTTGGAGAAGAGTGCGCT 420

QY  121 GTTGCAAAATCGTTCTTTTATAGTGTCTCATGATGTCATGCTGATGTTCTGATTT 180
    |||||||
DB  419 GTTGCAAAATCGTTCTTTTATAGTGTCTCATGATGTCATGCTGATGTTCTGATTT 360

QY  181 GTAGTTAAATCCTTTCCTCTCCGCGGTGAAATATACACAG 220
    |||||||
DB  359 GTAGTTAAATCCTTTCCTCTCCGCGGTGAAATATACACAG 320

RESULT 12
AAI99584
ID  AAI99584 standard; cDNA; 530 BP.
XX
AC  AAI99584;
XX
DT  04-JAN-2002 (first entry)
XX
DE  Human expressed polynucleotide SEQ ID NO 47.
XX
KW  Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;

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KW	immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnery;	PR	14-SEP-2000;	2000US-0233063
KW	antiparkinsonian; antisticking; antianaemic; antiathritic; cancer;	PR	14-SEP-2000;	2000US-0233064
KW	antiparkinsonian; antisticking; antianaemic; antiathritic; cancer;	PR	14-SEP-2000;	2000US-0233065
KW	antiallergic; hepatotropic; cerebroprotective; antinflammatory;	PR	21-SEP-2000;	2000US-0234272
KW	antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;	PR	21-SEP-2000;	2000US-0234273
KW	antiparastic; cardiac; immune disorder; cardiovascular disorder;	PR	25-SEP-2000;	2000US-0234397
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine;	PR	25-SEP-2000;	2000US-0234398
XX	ns.	PR	26-SEP-2000;	2000US-0235484
OS	Homo sapiens.	PR	27-SEP-2000;	2000US-0235834
XX		PR	27-SEP-2000;	2000US-0235836
XX		PR	29-SEP-2000;	2000US-0236327
XX		PR	29-SEP-2000;	2000US-0236367
XX		PR	29-SEP-2000;	2000US-0236368
XX		PR	29-SEP-2000;	2000US-0236369
XX		PR	29-SEP-2000;	2000US-0236370
XX		PR	02-OCT-2000;	2000US-0236802
XX		PR	02-OCT-2000;	2000US-0237037
XX		PR	02-OCT-2000;	2000US-0237038
XX		PR	02-OCT-2000;	2000US-0237039
XX		PR	02-OCT-2000;	2000US-0237040
XX		PR	13-OCT-2000;	2000US-0239335
XX		PR	13-OCT-2000;	2000US-0239337
XX		PR	20-OCT-2000;	2000US-0240960
XX		PR	20-OCT-2000;	2000US-0241221
XX		PR	20-OCT-2000;	2000US-0241785
XX		PR	20-OCT-2000;	2000US-0241786
XX		PR	20-OCT-2000;	2000US-0241877
XX		PR	20-OCT-2000;	2000US-0241878
XX		PR	20-OCT-2000;	2000US-0241879
XX		PR	20-OCT-2000;	2000US-0241880
XX		PR	20-OCT-2000;	2000US-0241881
XX		PR	20-OCT-2000;	2000US-0241882
XX		PR	20-OCT-2000;	2000US-0241883
XX		PR	20-OCT-2000;	2000US-0241884
XX		PR	20-OCT-2000;	2000US-0241885
XX		PR	20-OCT-2000;	2000US-0241886
XX		PR	20-OCT-2000;	2000US-0241887
XX		PR	20-OCT-2000;	2000US-0241888
XX		PR	20-OCT-2000;	2000US-0241889
XX		PR	20-OCT-2000;	2000US-0241890
XX		PR	20-OCT-2000;	2000US-0241891
XX		PR	20-OCT-2000;	2000US-0241892
XX		PR	20-OCT-2000;	2000US-0241893
XX		PR	20-OCT-2000;	2000US-0241894
XX		PR	20-OCT-2000;	2000US-0241895
XX		PR	20-OCT-2000;	2000US-0241896
XX		PR	20-OCT-2000;	2000US-0241897
XX		PR	20-OCT-2000;	2000US-0241898
XX		PR	20-OCT-2000;	2000US-0241899
XX		PR	20-OCT-2000;	2000US-0241900
XX		PR	20-OCT-2000;	2000US-0241901
XX		PR	20-OCT-2000;	2000US-0241902
XX		PR	20-OCT-2000;	2000US-0241903
XX		PR	20-OCT-2000;	2000US-0241904
XX		PR	20-OCT-2000;	2000US-0241905
XX		PR	20-OCT-2000;	2000US-0241906
XX		PR	20-OCT-2000;	2000US-0241907
XX		PR	20-OCT-2000;	2000US-0241908
XX		PR	20-OCT-2000;	2000US-0241909
XX		PR	20-OCT-2000;	2000US-0241910
XX		PR	20-OCT-2000;	2000US-0241911
XX		PR	20-OCT-2000;	2000US-0241912
XX		PR	20-OCT-2000;	2000US-0241913
XX		PR	20-OCT-2000;	2000US-0241914
XX		PR	20-OCT-2000;	2000US-0241915
XX		PR	20-OCT-2000;	2000US-0241916
XX		PR	20-OCT-2000;	2000US-0241917
XX		PR	20-OCT-2000;	2000US-0241918
XX		PR	20-OCT-2000;	2000US-0241919
XX		PR	20-OCT-2000;	2000US-0241920
XX		PR	20-OCT-2000;	2000US-0241921
XX		PR	20-OCT-2000;	2000US-0241922
XX		PR	20-OCT-2000;	2000US-0241923
XX		PR	20-OCT-2000;	2000US-0241924
XX		PR	20-OCT-2000;	2000US-0241925
XX		PR	20-OCT-2000;	2000US-0241926
XX				

	PR	08-DEC-2000; 2000US-0251868.
	PR	08-DEC-2000; 2000US-0251869.
	PR	08-DEC-2000; 2000US-0251989.
	PR	08-DEC-2000; 2000US-0251990.
	PR	11-DEC-2000; 2000US-0254097.
	PR	05-JAN-2001; 2001US-0259678.
	XX	
	PA	(HUMA-) HUMAN GENOME SCI INC.
	PI	Rosen CA, Barash SC, Ruben SM;
	DR	WPI: 2001-465573/50.
	P-PSDB:	AAM99972.
	PT	Isolated digestive system associated polypeptide for treating,
	PT	preventing and/or prognosing disorders related to the digestive system
	PT	including digestive system cancers and also for testing and detection
	e.g., diagnosis -	
	XX	
	PS	Claim 1; SEQ ID NO 47; 509pp + Sequence Listing; English.
	CC	The invention relates to novel genes (AAI99548-AAI99604) and proteins
	CC	(AAM99936-AAM99984) useful for preventing, treating or ameliorating
	CC	medical conditions e.g. by protein or gene therapy. The genes are
	CC	isolated from a range of human tissues disclosed in the specification.
	CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful
	CC	in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
	CC	and ovarian cancer and other cancers of the adrenal gland, bone, bone
	CC	marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
	CC	(b) immune disorders e.g. Addison's disease, allergies, autoimmune
	CC	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
	CC	disease, multiple sclerosis, rheumatoid arthritis and ulcerative
	CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias;
	CC	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
	CC	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
	CC	and parasitic infections.
	CC	Note: The sequence data for this patent did not form part of the
	CC	printed specification, but was obtained in electronic format directly
	CC	from WIPo at ftp.wipo.int/pub/published_pct.sequences.
	XX	
	SQ	Sequence 530 BP; 158 A; 105 C; 95 G; 171 T; 1 other;
	Query Match	51.8%; Score 166.4; DB 22; Length 530;
	Best Local Similarity	70.0%; Pred. No. 4.2e-40;
	Matches 224; Conservative	0; Mismatches 96; Indels 0; Gaps 0;
Oy	1	GGTGTAACCTTCGCTGGCTTCTCATCATTGTTGTTCCATAATCACTAGTGCTGTTGCC
Db	32	GATTATTAATTTGGCGCATTTATCATCAAGAATTTTCTTAGGAAGCAAGCTTTACT
Oy	61	ATTCAAACAACCCTTGAGAACCCACAGACAGTAAGGAATGTTTTGGAAGAGGCGCT
Db	92	GTTCAATCAAGAAGGCATTAACAGCACTGAAATPACGAAATCAAGTTAAAAAAGAGATC
Oy	121	GTTCGAAAATCGTTCTTTTATAGTGTTCTGTGATCCGATCGTGGATGTTCTGTATT
Db	152	CITGCCAACAAGTTTCTTTCTTATAGATTCTACTGATGATTTATGCGATACCATT
Oy	181	GATGTTAAATCTTTCCTCTTCGCGGGTGAAATPACAGACACAACTGCTCGGATA
Db	212	GATGGAATTTCTTCTACTGCTTCAAGGTAAGAAATACAGATACCATCACTCTGGTA
Oy	241	GATGATTTTTCCTTCACAGTTAAACAGTGTGTTGATCCATCTCTATACTTCACACC
Db	272	GTGATTTTATCTCCCATTAACAGTGCTTTGAACCCAAATTCCTATACCTGACACCA
Oy	301	AACTTTTAAAGACAAGTT 320
Db	332	AGACATTTAAAGAAATGAT 351

ID	AA13564	standard; cDNA; 530 BP.
XX		
AC	AA13564;	
XX		
DT	08-JAN-2002	(first entry)
XX		
DE	Human musculoskeletal system related polynucleotide seq ID NO 986.	
XX		
KW	Cytostatic; immunosuppressive; nocitropic; neuroprotective; antiviral;	
KW	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;	
KW	vulnerable; anticonvulsant; antibacterial; antitumor; antiparasitic;	
KW	cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;	
KW	neurological disease; infection; human; secreted protein;	
KW	musculoskeletal system; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200155367-A1.	
XX		
PD	02-AUG-2001.	
XX		
PF	17-JAN-2001;	2001WO-US01338.
XX		
PR	31-JAN-2000;	2000US-0179065.
PR	04-FEB-2000;	2000US-0180628.
PR	24-FEB-2000;	2000US-0184664.
PR	02-MAR-2000;	2000US-0186350.
PR	16-MAR-2000;	2000US-0189874.
PR	17-MAR-2000;	2000US-0190076.
PR	18-APR-2000;	2000US-0198123.
PR	19-MAY-2000;	2000US-0205515.
PR	07-JUN-2000;	2000US-0209467.
PR	28-JUN-2000;	2000US-0214886.
PR	30-JUN-2000;	2000US-0215135.
PR	07-JUL-2000;	2000US-0216647.
PR	07-JUL-2000;	2000US-0216880.
PR	11-JUL-2000;	2000US-0217487.
PR	11-JUL-2000;	2000US-0217496.
PR	14-JUL-2000;	2000US-0218290.
PR	26-JUL-2000;	2000US-0220963.
PR	26-JUL-2000;	2000US-0220964.
PR	14-AUG-2000;	2000US-0224518.
PR	14-AUG-2000;	2000US-0224519.
PR	14-AUG-2000;	2000US-0225213.
PR	14-AUG-2000;	2000US-0225214.
PR	14-AUG-2000;	2000US-0225266.
PR	14-AUG-2000;	2000US-0225267.
PR	14-AUG-2000;	2000US-0225268.
PR	14-AUG-2000;	2000US-0225270.
PR	14-AUG-2000;	2000US-0225447.
PR	14-AUG-2000;	2000US-0225757.
PR	14-AUG-2000;	2000US-0225758.
PR	14-AUG-2000;	2000US-0225759.
PR	18-AUG-2000;	2000US-0226279.
PR	22-AUG-2000;	2000US-0226681.
PR	22-AUG-2000;	2000US-0226688.
PR	22-AUG-2000;	2000US-0227182.
PR	23-AUG-2000;	2000US-0227009.
PR	30-AUG-2000;	2000US-0228924.
PR	01-SEP-2000;	2000US-0229287.
PR	01-SEP-2000;	2000US-0229343.
PR	01-SEP-2000;	2000US-0229344.
PR	01-SEP-2000;	2000US-0229345.
PR	05-SEP-2000;	2000US-0229509.
PR	05-SEP-2000;	2000US-0229513.
PR	06-SEP-2000;	2000US-0230437.
PR	06-SEP-2000;	2000US-0230438.
PR	08-SEP-2000;	2000US-0231242.
PR	08-SEP-2000;	2000US-0231243.
PR	08-SEP-2000;	2000US-0231244.
PR	08-SEP-2000;	2000US-0231413.
PR	08-SEP-2000;	2000US-0231414.
PR	08-SEP-2000;	2000US-0232080.



QY 301 AACCTTTTAAGACAAGTT 320  
| | | | | | | | | |  
Db 332 AGACCACTTTAAAGCAATGAT 351

RESULT 14  
ABA06471  
ID ABA06471 standard; cDNA; 530 BP.  
XX  
AC ABA06471;  
XX  
DT 10-JAN-2002 (first entry)  
XX  
DE Human cDNA SEQ ID NO: 137.  
XX  
KW Human; gene therapy; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW proliferative disorder; inflammation; ss.  
XX Homo sapiens.  
XX  
PN WO200154474-A2.  
PD 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01349.  
XX  
PR 31-JAN-2000; 2000US-179065P.  
PR 04-FEB-2000; 2000US-180628P.  
PR 24-FEB-2000; 2000US-184664P.  
PR 02-MAR-2000; 2000US-186350P.  
PR 16-MAR-2000; 2000US-189874P.  
PR 17-MAR-2000; 2000US-190076P.  
PR 18-APR-2000; 2000US-198123P.  
PR 19-MAY-2000; 2000US-205515P.  
PR 07-JUN-2000; 2000US-209467P.  
PR 28-JUN-2000; 2000US-214866P.  
PR 30-JUN-2000; 2000US-215135P.  
PR 07-JUL-2000; 2000US-216647P.  
PR 11-JUL-2000; 2000US-216880P.  
PR 11-JUL-2000; 2000US-217487P.  
PR 14-JUL-2000; 2000US-217496P.  
PR 14-JUL-2000; 2000US-218230P.  
PR 26-JUL-2000; 2000US-220963P.  
PR 14-AUG-2000; 2000US-220964P.  
PR 14-AUG-2000; 2000US-224518P.  
PR 14-AUG-2000; 2000US-224519P.  
PR 14-AUG-2000; 2000US-225213P.  
PR 14-AUG-2000; 2000US-225214P.  
PR 14-AUG-2000; 2000US-225266P.  
PR 14-AUG-2000; 2000US-225267P.  
PR 14-AUG-2000; 2000US-225268P.  
PR 14-AUG-2000; 2000US-225270P.  
PR 14-AUG-2000; 2000US-225447P.  
PR 14-AUG-2000; 2000US-225757P.  
PR 14-AUG-2000; 2000US-225758P.  
PR 14-AUG-2000; 2000US-225759P.  
PR 18-AUG-2000; 2000US-226279P.  
PR 22-AUG-2000; 2000US-226681P.  
PR 22-AUG-2000; 2000US-226686P.  
PR 22-AUG-2000; 2000US-227182P.  
PR 23-AUG-2000; 2000US-227009P.  
PR 30-AUG-2000; 2000US-228924P.  
PR 01-SEP-2000; 2000US-229287P.  
PR 01-SEP-2000; 2000US-229343P.  
PR 01-SEP-2000; 2000US-229344P.  
PR 01-SEP-2000; 2000US-229345P.  
PR 05-SEP-2000; 2000US-229509P.  
PR 05-SEP-2000; 2000US-229513P.  
PR 06-SEP-2000; 2000US-230437P.  
PR 06-SEP-2000; 2000US-230438P.

PR 08-SEP-2000; 2000US-231242P.  
PR 08-SEP-2000; 2000US-231243P.  
PR 08-SEP-2000; 2000US-231244P.  
PR 08-SEP-2000; 2000US-231413P.  
PR 08-SEP-2000; 2000US-231414P.  
PR 08-SEP-2000; 2000US-232080P.  
PR 08-SEP-2000; 2000US-232081P.  
PR 12-SEP-2000; 2000US-231968P.  
PR 14-SEP-2000; 2000US-232397P.  
PR 14-SEP-2000; 2000US-232398P.  
PR 14-SEP-2000; 2000US-232399P.  
PR 14-SEP-2000; 2000US-232400P.  
PR 14-SEP-2000; 2000US-232401P.  
PR 14-SEP-2000; 2000US-233063P.  
PR 14-SEP-2000; 2000US-233064P.  
PR 21-SEP-2000; 2000US-233065P.  
PR 21-SEP-2000; 2000US-234223P.  
PR 25-SEP-2000; 2000US-234274P.  
PR 25-SEP-2000; 2000US-234937P.  
PR 25-SEP-2000; 2000US-234938P.  
PR 26-SEP-2000; 2000US-235484P.  
PR 27-SEP-2000; 2000US-235834P.  
PR 27-SEP-2000; 2000US-235836P.  
PR 29-SEP-2000; 2000US-236327P.  
PR 29-SEP-2000; 2000US-236367P.  
PR 29-SEP-2000; 2000US-236368P.  
PR 29-SEP-2000; 2000US-236369P.  
PR 29-SEP-2000; 2000US-236370P.  
PR 02-OCT-2000; 2000US-237037P.  
PR 02-OCT-2000; 2000US-237038P.  
PR 02-OCT-2000; 2000US-237039P.  
PR 02-OCT-2000; 2000US-237040P.  
PR 13-OCT-2000; 2000US-239934P.  
PR 13-OCT-2000; 2000US-240960P.  
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PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI WPI: 2001-488777/53.  
XX P-PSDB: AAU18108.  
DR  
XX  
PT Isolated polypeptide and nucleic acid molecules for treating,  
PT preventing and/or prognosing disorders related to uterine motility  
XX e.g. disorders associated with pregnancy and the menstrual cycle -  
PS Claim 4; SEQ ID No 25; 524pp; English.  
XX  
CC The present invention relates to the isolation of novel human  
CC uterine motility-associated polypeptides (AAU18094-AAU18152),  
CC and cDNA and genomic sequences encoding for these polypeptides.  
CC The sequences of the invention are useful in the diagnosis,  
CC treatment, prevention and/or prognosis of diseases associated  
CC with uterine motility such as pregnancy and labour, and menstrual  
CC disorders. The polynucleotide sequences of the invention are also  
CC useful in gene therapy. AMS28936-AMS28994 represent cDNA sequences  
CC encoding for novel human uterine motility-associated polypeptides.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 530 BP; 158 A; 105 C; 95 G; 171 T; 1 other;  
Query Match 51.8%; Score 166.4; DB 22; Length 530;  
Best Local Similarity 70.0%; Pred. No. 4.2e-40;  
Matches 224; Conservative 0; Mismatches 96; Indels 0; Gaps 0;  
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QY 61 ATTCAAAAACCGCTTCAGACACAGAGTAAGAAATGTTTGAAGAGAGTGGCT 120  
DB 92 GTTCATCAAGTGCATTAACAGCAACGTAAATACGATCAAGTTAAAGAGATGATC 151  
QY 121 GTTGCAATGCTTTCTTTTATAGTGTCTGATGCAATCTGCTGATTCGTATTT 180  
DB 152 CTGGCAACGTTTTCTTTATATAGTACTGATGATTAATGCTGATGATCCCATTTT 211  
QY 181 GTAGTAAATCTTCCCTTCCTCCGGTGAAGAAATACAGCAACAAATCTTCCGATA 240  
DB 212 GTAGTAATTTCTTCTACCTGCTCAGTAGAATACAGGATACCATTAACCTCTGGGTA 271  
QY 241 GTGATTTTCTTCAGTAAAGTCTTGAATCCAAATCTATATCTCTCAACAC 300  
DB 272 GTGATTTTATTCGCAATTAACAGTCTTGAACCAATTCCTATATCTGACGACA 331  
QY 301 AACTTTTAAAGACAGTT 320  
DB 332 AGACATTTAAAGAAATGAT 351

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Job time : 244 secs

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	34.8	10.8	1831	1	US-08-101-433-3 Sequence 3, Appl
3	32.4	10.1	957	1	US-08-349-696-26 Sequence 26, Appl
4	32.4	10.1	957	1	US-08-233-009-26 Sequence 26, Appl
5	32.4	10.1	957	1	US-08-560-231-26 Sequence 26, Appl
6	32.4	10.1	957	4	US-09-080-704A-26 Sequence 26, Appl
7	30.8	9.6	1695	4	US-09-149-476-299 Sequence 299, App
8	30.6	9.5	51952	3	US-08-947-823-1 Sequence 1, Appl
9	30.2	9.4	7486	3	US-08-475-886-5 Sequence 5, Appl
10	30.2	9.4	7486	4	US-08-397-232-3 Sequence 3, Appl
11	30.2	9.4	7486	4	US-09-653-499-5 Sequence 5, Appl
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16	30	9.3	7521	4	US-09-004-838-116 Sequence 116, App
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18	29.8	9.3	1400	4	US-08-945-476-10 Sequence 10, Appl
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33	29.4	9.2	1302	3	US-09-122-632-3 Sequence 3, Appl
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35	29.4	9.2	4084	2	US-08-487-826B-1 Sequence 1, Appl
36	29.4	9.2	4084	4	US-09-210-288-1 Sequence 1, Appl
37	29.4	9.2	4084	6	5198347-5 Sequence 1, Appl
38	29.4	9.2	9909	4	US-08-961-527-12 Patent No: 5198347
39	29.2	9.1	2047	4	US-09-453-702B-222 Sequence 12, Appl
40	29	9.0	883	1	US-07-828-798C-4 Sequence 22, App
41	29	9.0	883	2	US-08-315-868A-4 Sequence 4, Appl
42	29	9.0	883	3	US-08-495-819B-4 Sequence 4, Appl
43	29	9.0	1882	1	US-08-458-120-1 Sequence 4, Appl
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45	29	9.0	1882	4	US-09-326-217-1 Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 869149  
INFORMATION FOR SEQ. ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: PTZ9PT-FLS  
US-08-232-463-14  
Query Match 12.7%; Score 40.8; DB 1; Length 7218;







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; Sequence 26, Application US/09080704A
; Patent No. 6166181
; GENERAL INFORMATION:
; APPLICANT: Jacobson, Marlene A
; APPLICANT: Johnson, Robert G
; APPLICANT: Luneau, Christopher J
; APPLICANT: Salvatore, Christopher A
; TITLE OF INVENTION: Human Adenosine Receptors
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: United States
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,704A
; FILING DATE: 18 May 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Parr, Richard S.
; REGISTRATION NUMBER: 32,586
; REFERENCE/DOCKET NUMBER: 18699DB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)594-4958
; TELEFAX: (732)594-4720
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 957 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-080-704A-26

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Best Local Similarity 49.1%; Pred. No. 2;
Matches 115; Conservative 0; Mismatches 116; Indels 3; Gaps 1;

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QY      203 TCCGGGTGGAATATGACAGACAAATGCTCGATAGTAGATTTTTCCTCCAGTTA 262
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
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; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057, 669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049, 610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061, 060
EARLIER FILING DATE: 1997-10-02

Query Match          9.6%; Score 30.8; DB 4; Length 1695;
Match Local Similarity 58.9%; Pred. No. 6.8;
Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 111 AGAGGTGCGTGTGGCAATCGTTCTTTTATGTTCTGTCGATCGCTGAT 170
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1382 AGAGTGGATGTTGGCATGTTGATATATTTACTAATATCTGATGATTTGTTTT 1441
QY 171 TCGTGTATTTGTAGTTAAATCCCTTTCCCT 200
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1442 TGCATTGGTTATGTTTTCCTTCCCTTTCCT 1471

RESULT 8
US-08-947-823-1/c
: Sequence 1, Application US/08947823
: Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isqouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

```

```
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-947-823-1

Query Match
Best Local Similarity: 9.5%; Score 30.6; DB 3; Length 51952;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 91 GTAGAGAAATGTTTGGAGAGAGAGGCTGTTGCAAAATGCTTTTATAGTGTTC 150
Db 23249 GTAGAAATTTCTTTTGTGTAGTGTCCGCGAGTGTATTTGTATGAGCTTTATAGCGAGA 23190

QY 151 TGTGATGCATGCTGTGATTCCTGTATTTGTAGTTAAAT 191
Db 23189 TGTGCGGCTAGCTGTTAACTTTGTTGTAGTTAAAT 23149

RESULT 9
US-08-475-886-5
Sequence 5, Application US/08475886A
Patent No. 6113912
GENERAL INFORMATION:
APPLICANT: FUNKHOUSER, ANN W
APPLICANT: EMERSON, SUZANNE U
APPLICANT: PURCELL, ROBERT H
APPLICANT: D'HONDT, ERIC
TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
FILE REFERENCE: 20264262US2
CURRENT APPLICATION NUMBER: US/08/475,886A
CURRENT FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 07/947,338
EARLIER FILING DATE: 1992-09-18
EARLIER APPLICATION NUMBER: 08/397,232
EARLIER FILING DATE: 1995-03-10
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 7486
TYPE: DNA
ORGANISM: Attenuated HAV (4380), strain HM-175
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FEATURE:
NAME/KEY: CDS
LOCATION: (730)..(7410)
US-08-475-886-5

Query Match
Best Local Similarity: 9.4%; Score 30.2; DB 3; Length 7486;
Matches 89; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 40 TATATTACTATGTTCTGCTTCATTCACAAAACCGCCTTGACAGCACAGAGTAAGGAAT 99
Db 7298 TTTATTATTGTTTGTACAGTCTGTTTGAGAGAGATGATGATACAGACTTAATCTT 7357

QY 100 TGTTTGGAGAGAGAGTGCTGTTGCAAAATCGTTTCTTTTATAGTGTCTGTATGCC 159
Db 7358 ATGATTGCTGAGAAATGAGATTTATGACAGGTTCATTGTGACCTTTCATGATTTG 7417

QY 160 ATCTGCTGATTCCTGATTTGTAGTTAAATCCTTCCTTCGCGGTGAATATCCA 219
Db 7418 TTTAAAGCAATTTCTTAAATTTGAGGTTGTTTATTTCTTTATATCAGTAATATAA 7477

QY 220 GACACAA 226
Db 7478 AAAAAA 7484

RESULT 10
US-08-397-232-3
Sequence 3, Application US/08397232A
Patent No. 6180110
GENERAL INFORMATION:
APPLICANT: FUNKHOUSER, ANN W
APPLICANT: EMERSON, SUZANNE U
APPLICANT: PURCELL, ROBERT H
APPLICANT: D'HONDT, ERIC
TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
FILE REFERENCE: 20264262US1
CURRENT APPLICATION NUMBER: US/08/397,232A
CURRENT FILING DATE: 1995-04-17
EARLIER APPLICATION NUMBER: 07/947,338
EARLIER FILING DATE: 1992-09-18
EARLIER APPLICATION NUMBER: PCT/US93/08610
EARLIER FILING DATE: 1993-09-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 7486
TYPE: DNA
ORGANISM: Attenuated HAV (4380), strain HM-175
FEATURE:
NAME/KEY: CDS
LOCATION: (730)..(7410)
US-08-397-232-3

Query Match
Best Local Similarity: 9.4%; Score 30.2; DB 4; Length 7486;
Matches 89; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 40 TATATTACTATGTTCTGCTTCATTCACAAAACCGCCTTGACAGCACAGAGTAAGGAAT 99
Db 7298 TTTATTATTGTTTGTACAGTCTGTTTGAGAGAGATGATGATACAGACTTAATCTT 7357

QY 100 TGTTTGGAGAGAGTGCTGTTGCAAAATCGTTTCTTTTATAGTGTCTGTATGCC 159
Db 7358 ATGATTGCTGAGAAATGAGATTTATGACAGGTTCATTGTGACCTTTCATGATTTG 7417

QY 160 ATCTGCTGATTCCTGATTTGTAGTTAAATCCTTCCTTCGCGGTGAATATCCA 219
Db 7418 TTTAAAGCAATTTCTTAAATTTGAGGTTGTTTATTTCTTTATATCAGTAATATAA 7477

QY 220 GACACAA 226
Db 7478 AAAAAA 7484
```

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RESULT 11
US-09-653-499-5
; Sequence 5, Application US/09653499
; Patent No. 6423318
; GENERAL INFORMATION:
; APPLICANT: FUNKHOUSER, ANN W
; APPLICANT: EMERSON, SUZANNE U
; APPLICANT: PURCELL, ROBERT H
; APPLICANT: D'HONDT, ERIC
; TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
; FILE REFERENCE: 20264262US2
; CURRENT APPLICATION NUMBER: US/09/653,499
; PRIOR APPLICATION NUMBER: 08/475,886
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: 07/947,338
; PRIOR FILING DATE: 1992-09-18
; PRIOR APPLICATION NUMBER: 08/397,232
; PRIOR FILING DATE: 1995-03-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7486
; TYPE: DNA
; ORGANISM: Attenuated HAV (4380), strain HM-175
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (730)..(7410)
US-09-653-499-5
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Query Match
Best Local Similarity 9.4%; Score 30.2; DB 4; Length 7486;
Matches 89; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 40 TATATTACTATGTTCTGTCATTCACAAAACCGCTTCGACACACAGAGTAAGAAAT 99
DB 7298 TTTATTATTGTTGTCAGTCCCTGTTGGAGAAAGATGATATACAGACTTAATCTT 7357
QY 100 TGTTTGGAAGAGAGTGCGTCTTCAATCGTTCTTTTATAGTGTCTGATGCC 159
DB 7358 ATGATTGGTGAGAAATGAGATTATGACCACTGTTTCATTTGTCACCTTCATGATTG 7417
QY 160 ATCTGCTGATTCCTGATTTGCTAGTAAATCCTTCCTCCGCGGTGAATATACA 219
DB 7418 TTTAAGCAATTTCTTTAAATTTCTGAGGTTGTTTATTCTTTATCAGTAATAAATA 7477
QY 220 GACACAA 226
DB 7478 AAAAAAA 7484
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```
RESULT 12
US-08-475-886-3
; Sequence 3, Application US/08475886A
; Patent No. 6113912
; GENERAL INFORMATION:
; APPLICANT: FUNKHOUSER, ANN W
; APPLICANT: EMERSON, SUZANNE U
; APPLICANT: PURCELL, ROBERT H
; APPLICANT: D'HONDT, ERIC
; TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
; FILE REFERENCE: 20264262US2
; CURRENT APPLICATION NUMBER: US/08/475,886A
; CURRENT FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 07/947,338
; EARLIER FILING DATE: 1992-09-18
; EARLIER APPLICATION NUMBER: 08/397,232
; EARLIER FILING DATE: 1995-03-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; LENGTH: 7488
; TYPE: DNA
; ORGANISM: Attenuated (Pass 35) HAV, strain HM-175
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (730)..(7410)
US-08-475-886-3
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Query Match
Best Local Similarity 9.4%; Score 30.2; DB 3; Length 7488;
Matches 89; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
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QY 40 TATATTACTATGTTCTGTCATTCACAAAACCGCTTCGACACACAGAGTAAGAAAT 99
DB 7298 TTTATTATTGTTGTCAGTCCCTGTTGGAGAAAGATGATATACAGACTTAATCTT 7357
QY 100 TGTTTGGAAGAGAGTGCGTCTTCAATCGTTCTTTTATAGTGTCTGATGCC 159
DB 7358 ATGATTGGTGAGAAATGAGATTATGACCACTGTTTCATTTGTCACCTTCATGATTG 7417
QY 160 ATCTGCTGATTCCTGATTTGCTAGTAAATCCTTCCTCCGCGGTGAATATACA 219
DB 7418 TTTAAGCAATTTCTTTAAATTTCTGAGGTTGTTTATTCTTTATCAGTAATAAATA 7477
QY 220 GACACAA 226
DB 7478 AAAAAAA 7484
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RESULT 13
US-09-653-499-3
; Sequence 3, Application US/09653499
; Patent No. 6423318
; GENERAL INFORMATION:
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; APPLICANT: FUNKHOUSER, ANN W
; APPLICANT: EMERSON, SUZANNE U
; APPLICANT: PURCELL, ROBERT H
; APPLICANT: D'HONDT, ERIC
; TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
; FILE REFERENCE: 20264262US2
; CURRENT APPLICATION NUMBER: US/09/653,499
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 08/475,886
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: 07/947,338
; PRIOR FILING DATE: 1992-09-18
; PRIOR APPLICATION NUMBER: 08/397,232
; PRIOR FILING DATE: 1995-03-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; LENGTH: 7488
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; TYPE: DNA
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; ORGANISM: Attenuated (Pass 35) HAV, strain HM-175
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; FEATURE:
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; NAME/KEY: CDS
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; LOCATION: (730)..(7410)
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US-09-653-499-3
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Query Match
Best Local Similarity 9.4%; Score 30.2; DB 4; Length 7488;
Matches 89; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
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QY 40 TATATTACTATGTTCTGTCATTCACAAAACCGCTTCGACACACAGAGTAAGAAAT 99
DB 7298 TTTATTATTGTTGTCAGTCCCTGTTGGAGAAAGATGATATACAGACTTAATCTT 7357
QY 100 TGTTTGGAAGAGAGTGCGTCTTCAATCGTTCTTTTATAGTGTCTGATGCC 159
DB 7358 ATGATTGGTGAGAAATGAGATTATGACCACTGTTTCATTTGTCACCTTCATGATTG 7417
QY 160 ATCTGCTGATTCCTGATTTGCTAGTAAATCCTTCCTCCGCGGTGAATATACA 219
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Db 7418 TTTAAACGAATTTCTTAAATTTCTGAGGTTTATTTCTTTATTCAGTAATAATAA 7477  
QY 220 GACACAA 226  
Db 7478 AAAAAA 7484

RESULT 14  
US-08-945-296-2  
; Sequence 2, Application US/08945296  
; Patent No. 5972609  
; GENERAL INFORMATION:  
; APPLICANT: Tinsley, Jonathon M  
; APPLICANT: Davies, Kay E  
; APPLICANT: Dennis, Carina  
; TITLE OF INVENTION: Ulrophin gene promoter  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye P.C.  
; STREET: 1100 No. 5972609th Glebe Road, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/945,296  
; FILING DATE: 22-OCT-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/00979  
; FILING DATE: 24-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9508236.8  
; FILING DATE: 24-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9526028.7  
; FILING DATE: 20-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ms Mary J Wilson  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 620-26  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1655 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-945-296-2

Query Match 9.3%; Score 30; DB 2; Length 1655;  
Best Local Similarity 49.1%; Pred. No. 11;  
Matches 108; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

QY 7 AACTTGGCGCTTTTCATCATGTGTGTTCTATATTAATGTTCTGTCATTCATA 66  
Db 1077 AAGTTGGTGGCTCGCGCCCTTCCAGGTTGGCCTTTGACTGTTTGTGTTGGCGGAA 1136  
QY 67 AAAACCGCCTTGCAGACACAGAGTAAGTAATGTTTGGAGAAGAGTGCT--GTTG 124  
Db 1137 CTACACAGCAGAGAGATTCAGCAAGTAAGGGCGTTTTCATCGGGGTCAATTCCTT 1196  
QY 125 CAAATCGTTCTTTTATTAATGTTCTCTGATGCCATCTGCTGATTCCTGATTTAG 184  
Db 1197 TCTTCTTCTTTTAAATTTCCGTTCTGCTCTCTCCAAAGCTTAATTTT 1256  
QY 185 TTAATATCCTTCCCTCTCCGGGTGGAATACAGACAC 224

Db 1257 TTAATATCAGTCGACACACCAACTAACACTCGACACAC 1296

RESULT 15  
US-09-405-112-2  
; Sequence 2, Application US/09405112  
; Patent No. 6087111  
; GENERAL INFORMATION:  
; APPLICANT: Tinsley, Jonathon M  
; APPLICANT: Davies, Kay E  
; APPLICANT: Dennis, Carina  
; TITLE OF INVENTION: Ulrophin gene promoter  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye P.C.  
; STREET: 1100 No. 6087111th Glebe Road, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/405,112  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/945,296  
; FILING DATE: 22-OCT-1997  
; APPLICATION NUMBER: PCT/GB96/00979  
; FILING DATE: 24-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9508236.8  
; FILING DATE: 24-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9526028.7  
; FILING DATE: 20-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ms Mary J Wilson  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 620-26  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1655 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-09-405-112-2

Query Match 9.3%; Score 30; DB 3; Length 1655;  
Best Local Similarity 49.1%; Pred. No. 11;  
Matches 108; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

QY 7 AACTTGGCGCTTTTCATCATGTGTGTTCTATATTAATGTTCTGTCATTCATA 66  
Db 1077 AAGTTGGTGGCTCGCGCCCTTCCAGGTTGGCCTTTGACTGTTTGTGTTGGCGGAA 1136  
QY 67 AAAACCGCCTTGCAGACACAGAGTAAGTAATGTTTGGAGAAGAGTGCT--GTTG 124  
Db 1137 CTACACAGCAGAGAGATTCAGCAAGTAAGGGCGTTTTCATCGGGGTCAATTCCTT 1196  
QY 125 CAAATCGTTCTTTTATTAATGTTCTCTGATGCCATCTGCTGATTCCTGATTTAG 184  
Db 1197 TCTTCTTCTTTTAAATTTCCGTTCTGCTCTCTCCAAAGCTTAATTTT 1256  
QY 185 TTAATATCCTTCCCTCTCCGGGTGGAATACAGACAC 224

Db 1257 TTAATAATACATCGCACACCAAACTAACACTCGCACACAC 1296

Search completed: May 26, 2003, 20:05:41  
Job time : 110 secs

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QY	1	GGTGTGAACGTGCGGCTTTTTCATCATATGTGTTTCCATPATACTAATGTTCTGTCC	60
Db	1	GGTGTGACCTGCTGCGCTTTTCTCATATGTGTTTCCATPATACTAATGTTCTGTCC	60
QY	61	ATTCAAAAAACCGCTTGCAGACACACAGAAATGATTGTTTGGACAAGAGTGCGT	120
Db	61	ATTCAAAAAACCGCTTGCAGACACACAGAAATGATTGTTTGGACAAGAGTGCGT	120
QY	121	GTTTGCAAATGCTTTCTTTTATAGTGTCTCTGATGCCATCTGCTGGATTCTGATTTT	180
Db	121	GTTTGCAAATGCTTTCTTTTATAGTGTCTCTGATGCCATCTGCTGGATTCTGATTTT	180
QY	181	GTAATTAATAATCCCTTTCCCTTCCTCCGGGTGGAAATACACAGCAATAGATCTTCGTATA	240
Db	181	GTAATTAATAATCCCTTTCCCTTCCTCCGGGTGGAAATACACAGCAATAGATCTTCGTATA	240
QY	241	GTCATTTTTTCCCTCCAGTTAACAGTGCCTTGAATCAATCCCTCTTACTCTCACAAAC	300
Db	241	GTCATTTTTTCCCTCCAGTTAACAGTGCCTTGAATCAATCCCTCTTACTCTCACAAAC	300

RESULT 3  
US-09-965-536A-5  
Sequence 5, Application US/09965536A  
Publication No. US20030027323A1  
GENERAL INFORMATION:  
APPLICANT: FEDER, J. N.  
APPLICANT: MINTIER, G.

```

; LENGTH: 2193
; TYPE: DNA

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ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2190)  
NAME/KEY: sig\_peptide  
LOCATION: (1)..(108)  
US-09-928-175-6

Query Match  
Best Local Similarity 100.0%; Score 321; DB 10; Length 2193;  
Pred. No. 6,1e-85;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGGAACCTGCTGGCTTTCTCATCATGTTGTTTCTATATCTATGTTCTGTTCC 60  
DB 1714 GGTGGAACCTGCTGGCTTTCTCATCATGTTGTTTCTATATCTATGTTCTGTTCC 1773  
QY 61 ATTCAAAAACCGCTTCACACACACAGAAATGTAAGATTTGTTGGAAGAGGTGGCT 120  
DB 1774 ATTCAAAAACCGCTTCACACACACAGAAATGTAAGATTTGTTGGAAGAGGTGGCT 1833  
QY 121 GTTGCAATCGTTCTTTTATAGTGTCTGATGCAATGCTGATTCCTGATTT 180  
DB 1834 GTTGCAATCGTTCTTTTATAGTGTCTGATGCAATGCTGATTCCTGATTT 1893  
QY 181 GTAGTAAATCCCTTCCCTTCGCGGTGAATACACAGACAAATGACTTCTGATA 240  
DB 1894 GTAGTAAATCCCTTCCCTTCGCGGTGAATACACAGACAAATGACTTCTGATA 1953  
QY 241 GTGATTTTTCCTCCAGTAACAGTGTGAATCCATCCCTATCTACACACC 300  
DB 1954 GTGATTTTTCCTCCAGTAACAGTGTGAATCCATCCCTATCTACACACC 2013  
QY 301 AACTTTTTTAAGACAAGTTG 321  
DB 2014 AACTTTTTTAAGACAAGTTG 2034

RESULT 5  
US-09-965-536A-1  
Sequence 1, Application US/09965536A.  
Publication No. US20030027323A1  
GENERAL INFORMATION:

APPLICANT: FEDER, J. N.  
APPLICANT: MINTIER, G.  
APPLICANT: RAMANATHAN, C. S.  
APPLICANT: HAWKEN, D. R.  
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGRBRMYS,  
TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES  
FILE REFERENCE: D0041NP  
CURRENT APPLICATION NUMBER: US/09/965,536A  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/235,713  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/261,781  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/306,605  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: 60/310,436  
PRIOR FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2214  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-965-536A-1

Query Match  
Best Local Similarity 100.0%; Score 321; DB 9; Length 2214;  
Pred. No. 6,1e-85;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTGGAACCTGCTGGCTTTCTCATCATGTTGTTTCTATATCTATGTTCTGTTCC 60  
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DB 1735 GGTGGAACCTGCTGGCTTTCTCATCATGTTGTTTCTATATCTATGTTCTGTTCC 1794

QY 61 ATTCAAAAACCGCTTCACACACACAGAAATGTAAGATTTGTTGGAAGAGGTGGCT 120  
DB 1795 ATTCAAAAACCGCTTCACACACACAGAAATGTAAGATTTGTTGGAAGAGGTGGCT 1854

QY 121 GTTGCAATCGTTCTTTTATAGTGTCTGATGCAATGCTGATTCCTGATTT 180  
DB 1855 GTTGCAATCGTTCTTTTATAGTGTCTGATGCAATGCTGATTCCTGATTT 1914

QY 181 GTAGTAAATCCCTTCCCTTCGCGGTGAATACACAGACAAATGACTTCTGATA 240  
DB 1915 GTAGTAAATCCCTTCCCTTCGCGGTGAATACACAGACAAATGACTTCTGATA 1974

QY 241 GTGATTTTTCCTCCAGTAACAGTGTGAATCCATCCCTATCTACACACC 300  
DB 1975 GTGATTTTTCCTCCAGTAACAGTGTGAATCCATCCCTATCTACACACC 2034

QY 301 AACTTTTTTAAGACAAGTTG 321  
DB 2035 AACTTTTTTAAGACAAGTTG 2055

RESULT 6  
US-09-928-175-1  
Sequence 1, Application US/09928175  
Patent No. US20020123618A1  
GENERAL INFORMATION:

APPLICANT: Paszly, Christopher J.  
APPLICANT: Gong, Jianhua  
APPLICANT: Daugherty, Betsy  
APPLICANT: Rogers, No. US20020123618A1ma  
TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and  
TITLE OF INVENTION: Uses Thereof  
FILE REFERENCE: 00-1229  
CURRENT APPLICATION NUMBER: US/09/928,175  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/224,455  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 2265  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2262)  
NAME/KEY: sig\_peptide  
LOCATION: (1)..(108)  
US-09-928-175-1

Query Match  
Best Local Similarity 100.0%; Score 321; DB 10; Length 2265;  
Pred. No. 6,2e-85;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGGAACCTGCTGGCTTTCTCATCATGTTGTTTCTATATCTATGTTCTGTTCC 60  
DB 1786 GGTGGAACCTGCTGGCTTTCTCATCATGTTGTTTCTATATCTATGTTCTGTTCC 1845

QY 61 ATTCAAAAACCGCTTCACACACACAGAAATGTAAGATTTGTTGGAAGAGGTGGCT 120  
DB 1846 ATTCAAAAACCGCTTCACACACACAGAAATGTAAGATTTGTTGGAAGAGGTGGCT 1905

QY 121 GTTGCAATCGTTCTTTTATAGTGTCTGATGCAATGCTGATTCCTGATTT 180  
DB 1906 GTTGCAATCGTTCTTTTATAGTGTCTGATGCAATGCTGATTCCTGATTT 1965

QY 181 GTAGTAAATCCCTTCCCTTCGCGGTGAATACACAGACAAATGACTTCTGATA 240  
DB 1966 GTAGTAAATCCCTTCCCTTCGCGGTGAATACACAGACAAATGACTTCTGATA 2025

QY 241 GTGATTTTTCCTCCAGTAACAGTGTGAATCCATCCCTATCTACACACC 300  
|||||

Db 2026 GTGATTTTTCCTCCAGTTAACAGTGTGATCCATCCCTATCTACCTCACAACC 2085  
QY 301 AACTTTTAAAGACAGTGTG 321  
Db 2086 AACTTTTAAAGACAGTGTG 2106

## RESULT 7

US-10-229-735-2  
; Sequence 2, Application US/10229735  
; Publication No. US20030082650A1  
; GENERAL INFORMATION:  
; APPLICANT: Baylor College of Medicine  
; APPLICANT: Agoulrik, Alexander I.  
; TITLE OF INVENTION: The Great Gene and Protein  
; FILE REFERENCE: 7572/73263  
; CURRENT APPLICATION NUMBER: US/10/229,735  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/315,696  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/351,432  
; PRIOR FILING DATE: 2002-01-28  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 2436  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-229-735-2

Query Match 100.0%; Score 321; DB 9; Length 2436;  
Best Local Similarity 100.0%; Pred. No. 6,4e-85;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTGACTTGGCGCTTTCATCATGTGTTCCTATATCTACTAGTCTGTCC 60  
Db 1856 GGTGTGACTTGGCGCTTTCATCATGTGTTCCTATATCTACTAGTCTGTCC 1915  
QY 61 ATTCAAAAACCGCCTTCGACAGACACAGAGTAAGATTGTTTGGAGAGAGTGGCT 120  
Db 1916 ATTCAAAAACCGCCTTCGACAGACACAGAGTAAGATTGTTTGGAGAGAGTGGCT 1975  
QY 121 GTTGCAATGCTTCTTTTATAGTGTCTCTGATGCCATCTGCTGATTT 180  
Db 1976 GTTGCAATGCTTCTTTTATAGTGTCTCTGATGCCATCTGCTGATTT 2035  
QY 181 GTAGTAAATCCTTCCCTCCGCTGCGGTGGAATACACAGACAAATGACTTCTGGATA 240  
Db 2036 GTAGTAAATCCTTCCCTCCGCTGCGGTGGAATACACAGACAAATGACTTCTGGATA 2095  
QY 241 GTGATTTTTCCTCCAGTTAACAGTGTGATCCATCCCTATCTACCTCACAACC 300  
Db 2096 GTGATTTTTCCTCCAGTTAACAGTGTGATCCATCCCTATCTACCTCACAACC 2155  
QY 301 AACTTTTAAAGACAGTGTG 321  
Db 2156 AACTTTTAAAGACAGTGTG 2176

## RESULT 8

US-10-222-668-1  
; Sequence 1, Application US/10222668  
; Publication No. US2003008884A1  
; GENERAL INFORMATION:  
; APPLICANT: Hsu, Sheau Yu  
; APPLICANT: Hsueh, Aaron  
; TITLE OF INVENTION: Mammalian Relaxin Receptor  
; FILE REFERENCE: STAN-239 WO  
; CURRENT APPLICATION NUMBER: US/10/222,668  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/313,259  
; PRIOR FILING DATE: 2002-08-17

; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2838  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (107)...(2369)  
US-10-222-668-1

Query Match 100.0%; Score 321; DB 9; Length 2838;  
Best Local Similarity 100.0%; Pred. No. 6,9e-85;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTGACTTGGCGCTTTCATCATGTGTTCCTATATCTACTAGTCTGTCC 60  
Db 1892 GGTGTGACTTGGCGCTTTCATCATGTGTTCCTATATCTACTAGTCTGTCC 1951  
QY 61 ATTCAAAAACCGCCTTCGACAGACACAGAGTAAGATTGTTTGGAGAGAGTGGCT 120  
Db 1952 ATTCAAAAACCGCCTTCGACAGACACAGAGTAAGATTGTTTGGAGAGAGTGGCT 2011  
QY 121 GTTGCAATGCTTCTTTTATAGTGTCTCTGATGCCATCTGCTGATTT 180  
Db 2012 GTTGCAATGCTTCTTTTATAGTGTCTCTGATGCCATCTGCTGATTT 2071  
QY 181 GTAGTAAATCCTTCCCTCCGCTGCGGTGGAATACACAGACAAATGACTTCTGGATA 240  
Db 2072 GTAGTAAATCCTTCCCTCCGCTGCGGTGGAATACACAGACAAATGACTTCTGGATA 2131  
QY 241 GTGATTTTTCCTCCAGTTAACAGTGTGATCCATCCCTATCTACCTCACAACC 300  
Db 2132 GTGATTTTTCCTCCAGTTAACAGTGTGATCCATCCCTATCTACCTCACAACC 2191  
QY 301 AACTTTTAAAGACAGTGTG 321  
Db 2192 AACTTTTAAAGACAGTGTG 2212

## RESULT 9

US-09-928-175-19  
; Sequence 19, Application US/09928175  
; Patent No. US20020123618A1  
; GENERAL INFORMATION:  
; APPLICANT: Paszty, Christopher J.  
; APPLICANT: Gong, Jianhua  
; APPLICANT: Daugherty, Betsy  
; APPLICANT: Rogers, No. US20020123618A1ma  
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and  
; FILE REFERENCE: 00-1229  
; CURRENT APPLICATION NUMBER: US/09/928,175  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/224,455  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 2214  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..  
; NAME/KEY: sig\_peptide  
; LOCATION: (1)..  
US-09-928-175-19

Query Match 72.6%; Score 233; DB 10; Length 2214;  
Best Local Similarity 82.9%; Pred. No. 6,9e-59;  
Matches 266; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 GGTGTAACCTGCTGGCTTTTCATCATATGTTTCTATATATGTTCTGTTCC 60  
|||||  
Db 1735 GGTGTAACCTGCTGGCTTTTCATCATATGTTTCTATATATGTTCTGTTCC 1794  
QY 61 ATTCAAAAACCGCCTTCAGACACCAAGTAAGTAATTTTGGAGAGAGTGCT 120  
|||||  
Db 1795 ATTCAAAAACCGCCTTCAGACACCAAGTAAGTAATTTTGGAGAGAGTGCT 1854  
QY 121 GTTCAAAATCGTTTCTTTTATAGTGTCTGTATGTCATCTGTGATTCCTGATTT 180  
|||||  
Db 1855 GTTCAAAACCGCTTTCTTTTATAGTGTCTGTATGTCATCTGTGATTCCTGATTT 1914  
QY 181 GTAGTAAATCCCTTCCCTCCGCGGTAATACCAAGACAAATGACTCTCGATTA 240  
|||||  
Db 1915 GTGCTTAAGATCGTGTCTCTCCTTCAAGTGTGAGATACGAGCAATCATCTCGGATC 1974  
QY 241 GTGATTTTTTCTTCCAGTTAAGAGTCTTTGAATCCATCTCTATCTCTACAAC 300  
|||||  
Db 1975 GTGATTTTTTCTTCCAGTTAAGAGTCTTTGAATCCATCTCTATCTCTACAAC 2034  
QY 301 AACTTTTTTAAGACAAGTTG 321  
|||||  
Db 2035 TCCTTTTTTAAGACAAGTTG 2055

RESULT 10  
US-10-229-735-4  
; Sequence 4, Application US/10229735  
; Publication No. US20030082650A1  
; GENERAL INFORMATION:  
; APPLICANT: Baylor College of Medicine  
; APPLICANT: Agoulrik, Alexander I.  
; TITLE OF INVENTION: The GREAT Gene and Protein  
; FILE REFERENCE: 7572/73263  
; CURRENT APPLICATION NUMBER: US/10/229,735  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/315,696  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/351,432  
; PRIOR FILING DATE: 2002-01-28  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 2539  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-229-735-4

Query Match 72.6%; Score 233; DB 9; Length 2539;  
Best Local Similarity 82.9%; Pred. No. 7.3e-59;  
Matches 266; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 GGTGTAACCTGCTGGCTTTTCATCATATGTTTCTATATATGTTCTGTTCC 60  
|||||  
Db 1928 GGTGTAACCTGCTGGCTTTTCATCATATGTTTCTATATATGTTCTGTTCC 1987  
QY 61 ATTCAAAAACCGCCTTCAGACACCAAGTAAGTAATTTTGGAGAGAGTGCT 120  
|||||  
Db 1988 ATTCAAAAACCGCCTTCAGACACCAAGTAAGTAATTTTGGAGAGAGTGCT 2047  
QY 121 GTTCAAAATCGTTTCTTTTATAGTGTCTGTATGTCATCTGTGATTCCTGATTT 180  
|||||  
Db 2048 GTTCAAAACCGCTTTCTTTTATAGTGTCTGTATGTCATCTGTGATTCCTGATTT 2107  
QY 181 GTAGTAAATCCCTTCCCTCCGCGGTAATACCAAGACAAATGACTCTCGATTA 240  
|||||  
Db 2108 GTGCTTAAGATCGTGTCTCTCCTTCAAGTGTGAGATACGAGCAATCATCTCGGATC 2167  
QY 241 GTGATTTTTTCTTCCAGTTAAGAGTCTTTGAATCCATCTCTATCTCTACAAC 300  
|||||  
Db 2168 GTGATTTTTTCTTCCAGTTAAGAGTCTTTGAATCCATCTCTATCTCTACAAC 2227  
QY 301 AACTTTTTTAAGACAAGTTG 321

Db 2228 TCCTTTTTTAAGACAAGTTG 2248  
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RESULT 11  
US-09-782-974C-65/C  
; Sequence 65, Application US/09782974C  
; Publication No. US20030082534A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogel, Gabriel  
; APPLICANT: Lind, Peter  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Parodi, Luis A.  
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor  
; FILE REFERENCE: 411USPHW311  
; CURRENT APPLICATION NUMBER: US/09/782,974C  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 60/165,838  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 09/714,449  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 60/198,568  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 60/166,071  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,678  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: 60/173,396  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/184,129  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/185,421  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/185,554  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/186,530  
; PRIOR FILING DATE: 2000-03-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 65  
; LENGTH: 1018  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-782-974C-65

Query Match 68.5%; Score 220; DB 9; Length 1018;  
Best Local Similarity 100.0%; Pred. No. 3.4e-55;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTAACCTGCTGGCTTTTCATCATATGTTTCTATATATGTTCTGTTCC 60  
|||||  
Db 539 GGTGTAACCTGCTGGCTTTTCATCATATGTTTCTATATATGTTCTGTTCC 480  
QY 61 ATTCAAAAACCGCCTTCAGACACCAAGTAAGTAATTTTGGAGAGAGTGCT 120  
|||||  
Db 479 ATTCAAAAACCGCCTTCAGACACCAAGTAAGTAATTTTGGAGAGAGTGCT 420  
QY 121 GTTCAAAATCGTTTCTTTTATAGTGTCTGTATGTCATCTGTGATTCCTGATTT 180  
|||||  
Db 419 GTTCAAAATCGTTTCTTTTATAGTGTCTGTATGTCATCTGTGATTCCTGATTT 360  
QY 181 GTAGTAAATCCCTTCCCTCCGCGGTAATACCAAGTAATGACTCTCGATTT 220  
|||||  
Db 359 GTAGTAAATCCCTTCCCTCCGCGGTAATACCAAG 320

RESULT 12  
US-09-989-442-33  
; Sequence 33, Application US/09989442  
; Publication No. US20030013649A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PJZ08  
PRIOR APPLICATION NUMBER: US/09/989,442  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/214,886  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/217,487  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,758  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,963  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/217,496  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,447  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/218,290  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/225,757  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/226,868  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/216,647  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,267  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/216,880  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,270  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/251,869  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/235,834  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/234,274  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/224,223  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/228,924  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/224,518  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,369  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/224,519  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,964  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/241,809  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/249,299  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/236,327  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/241,785  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/244,617  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 60/225,268  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,368  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/251,856  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/251,868  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/229,344  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/234,997

PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: 60/229,343  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,345  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,287  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,513  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/231,413  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/229,509  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/236,367  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/237,039  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,038  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/236,370  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/236,802  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,037  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,040  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/240,960  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/239,935  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/239,937  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/241,787  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,474  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/246,532  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/249,216  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,210  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/226,681  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,759  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/225,213  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/227,182  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,214  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/235,836  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/230,438  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/215,135  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/225,266  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/249,218  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,208  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,213  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,212  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,207  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,245  
PRIOR FILING DATE: 2000-11-17

[illegible]

69-CTC-30T-0T-50

```

RESULT 14
US-10-103-313-89
: Sequence 89, Application US/10103313
: Publication No. US20030082756A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PJ207C1
: CURRENT APPLICATION NUMBER: US/10/103,313
: CURRENT FILING DATE: 2002-03-12
: NUMBER OF SEQ ID NOS: 653
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 89
: LENGTH: 530
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-103-313-89

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Query Match 51.8%; Score 166.4; DB 9; Length 530;  
Best Local Similarity 70.0%; Pred. No. 1.8e-39;  
Matches 224; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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QY 1 GGTGTGAACCTGCTGGCTTTTCATCATGTGTGTTTCCATATTAATGTTCTGTCC 60
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Db 32 GGTATTAATTTGGCCGATTTATCATCATAGTTTTCATAGAACCATGTTTATAGT 91
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 ATTCAAAAACCCCTTCGACACACAGAGTAAGAAATGTTTGGAGAGAGAGTGCT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 92 GTTCATCAAAAGTGCATTAACAGACAGTAAGTAAGCAATGTAAGTAAGTAAGTATC 151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 GTTGCAAAATGCTTTCTTTTATAGTGTCTGATGCCATCTGCTGATCTGTAATTT 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 152 CTGGCCAAAGCTTTTCTTTATAGTATGATGATGATGATGATGATGATGATGATGAT 211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GTAGTAAATCCCTTCCCTCCGAGGAAATACAGACAAATGATGATGATGATGATGATGAT 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 212 GTAGTAAATCTTCTTCTGCTTCAAGTAGAATACAGTAAGTAAGTAAGTAAGTAAGTAAG 271
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GTGATTTTCTTCTGCTTCAAGTAGAATGCTTGAATGCAATGCTTATGCTGACAAAC 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 GTGATTTTCTTCTGCTTCAAGTAGAATGCTTGAATGCAATGCTTATGCTGACAAAC 331
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 AACTTTTAAAGACAGTT 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 AGACATTTAAAGAAATGAT 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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## RESULT 15

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US-09-764-853-137
; Sequence 137, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-764-853-137
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Query Match 51.8%; Score 166.4; DB 10; Length 530;  
Best Local Similarity 70.0%; Pred. No. 1.8e-39;  
Matches 224; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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QY 1 GGTGTGAACCTGCTGGCTTTTCATCATGTGTGTTTCCATATTAATGTTCTGTCC 60
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Db 32 GGTATTAATTTGGCCGATTTATCATCATAGTTTTCATAGAACCATGTTTATAGT 91
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 ATTCAAAAACCCCTTCGACACACAGAGTAAGAAATGTTTGGAGAGAGAGTGCT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 92 GTTCATCAAAAGTGCATTAACAGACAGTAAGTAAGCAATGTAAGTAAGTAAGTATC 151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 GTTGCAAAATGCTTTCTTTTATAGTGTCTGATGCCATCTGCTGATCTGTAATTT 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 152 CTGGCCAAAGCTTTTCTTTATAGTATGATGATGATGATGATGATGATGATGATGAT 211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GTAGTAAATCCCTTCCCTCCGAGGAAATACAGACAAATGATGATGATGATGATGATGAT 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 212 GTAGTAAATCTTCTTCTGCTTCAAGTAGAATACAGTAAGTAAGTAAGTAAGTAAGTAAG 271
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GTGATTTTCTTCTGCTTCAAGTAGAATGCTTGAATGCAATGCTTATGCTGACAAAC 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 GTGATTTTCTTCTGCTTCAAGTAGAATGCTTGAATGCAATGCTTATGCTGACAAAC 331
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

QY 301 AACTTTTAAAGACAGTT 320  
Db 332 AGACATTTAAAGAAATGAT 351

Search completed: May 26, 2003, 20:07:59  
Job time: 181 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM nucleic - nucleic search, using sw model

Run on: May 26, 2003, 18:40:32 ; Search time 1741 Seconds  
(Without alignments)  
2986.072 Million cell updates/sec

Title: US-09-930-312-1

Perfect score: 321

Sequence: 1 ggtgtgactgtgctt.....acttttaagacaagttg 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:\*

- 1: em\_estda:\*
- 2: em\_esthum:\*
- 3: em\_estlin:\*
- 4: em\_estnu:\*
- 5: em\_estoy:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_estl:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_est3:\*
- 12: gb\_est4:\*
- 13: gb\_est5:\*
- 14: gb\_est6:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vit:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_man:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186.2	58.0	197	12	BF942735 EST-CD15N
2	159	49.5	841	14	BQ228832 AGENCOURT
3	154.6	48.2	744	12	BG304121 F130F05.X
4	152	47.4	235	10	AMA36170 75600 MAR
5	77.4	24.1	456	12	BF021857 uY58h08.Y
6	77.4	24.1	574	10	BB632910 BB632910

C	7	43.2	13.5	1100	17	CNS016W7	AL107281 Drosophila
	8	40.6	12.6	992	17	CNS04L30	AL295629 Tetradon
	9	40	12.5	660	17	BH46416	BH46416 BOPR39TR
C	10	39.2	12.2	1101	17	CNS00BEG	AL056872 Drosophila
	11	39	12.1	1024	17	CNS015ZE	AL106100 Drosophila
	12	38.2	11.9	681	17	AG148351	AG148351 Pan trogl
C	13	38	11.8	1073	9	AL551397	AL551397 F. rubripes
	14	37.8	11.8	598	17	FR0020632	AL013515 F. rubripes
C	15	37.6	11.8	1201	17	CNS016CF	AL106569 Drosophila
	16	37.6	11.7	1101	17	CNS0039G	AL063921 Drosophila
C	17	37.4	11.7	312	12	BF368833	BF368833 RCI-GN007
	18	37.4	11.7	480	9	AJ460181	AJ460181 AJ460181
C	19	37.4	11.7	624	10	AV929568	AV929568 AV929568
C	20	37.4	11.7	629	14	BQ465627	BQ465627 HU04D09r
C	21	37.2	11.6	441	9	AL369230	AL369230 MBR29P09
	22	37.2	11.6	537	14	BM780117	BM780117 EST390693
C	23	37.2	11.6	654	10	BE239472	BE239472 EST403521
	24	37.2	11.6	887	14	BM779689	BM779689 EST590265
C	25	37	11.5	1092	17	CNS020K7	AL175696 Tetradon
C	26	37	11.5	1433	12	BG247718	BG247718 602359413
C	27	36.8	11.5	619	17	FR0020635	AL013518 F. rubripes
C	28	36.8	11.5	678	10	AW984751	AW984751 RCI-HN001
	29	36.6	11.4	1201	17	CNS0107Y	AL098633 Drosophila
C	30	36.4	11.3	595	13	BM370473	BM370473 EBR008_SQ
C	31	36.4	11.3	877	12	BF208790	BF208790 601872268
C	32	36.4	11.3	949	17	CNS073SC	AL427906 clone BA0
C	33	36.2	11.3	267	9	AA939376	AA939376 on34d12.S
	34	36.2	11.3	586	10	AV944500	AV944500 AV944500
C	35	36.2	11.2	621	13	BJ484370	BJ484370 BJ484370
C	36	36	11.2	538	13	BJ062617	BJ062617 BJ062617
C	37	35.8	11.2	624	13	BJ060185	BJ060185 BJ060185
C	38	35.8	11.2	507	14	BQ313904	BQ313904 OV3-BN014
C	39	35.8	11.2	515	9	AL789330	AL789330 AL789330
C	40	35.8	11.2	797	17	BH122046	BH122046 RPT-24-3
C	41	35.8	11.2	902	17	CNS00CVM	AL060007 Drosophila
C	42	35.6	11.1	360	9	AJ460183	AJ460183 AJ460183
C	43	35.6	11.1	519	14	BM960895	BM960895 c1ha3E13S
C	44	35.6	11.1	663	12	BG450476	BG450476 NF019E01D
C	45	35.6	11.1	691	12	BG451906	BG451906 NP101C08D

## ALIGNMENTS

RESULT 1  
LOCUS BF942735  
DEFINITION EST-CD15N-040 human CD15+ myeloid progenitor cells cDNA library  
ACCESSION BF942735  
VERSION BF942735.1 GI:15624134  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 197)  
AUTHORS Chen, J., Lee, S., Zhou, G., Rowley, J. D. and Wang, S. M.  
TITLE A high-throughput GLGI procedure for converting large number of SAGE tag sequences into 3' ESTs  
JOURNAL Unpublished (2001)  
COMMENT Contact: Wang SM  
Hem/Onc

University of Chicago Medical Center  
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA  
Tel: 773-702-6788  
Fax: 773-702-3002  
Email: swang1@midway.uchicago.edu  
This EST fragment was amplified from human CD15+ myeloid progenitor cells cDNA library with GLGI technique (Generation of Longer cDNA fragments from SAGE tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till the last CATG site of the target cDNA sequence.

```

Seq primer: M13 Forward.
FEATURES
    source          location/Qualifiers
                    1..197
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone_idb="human CD15+ myeloid progenitor cells cDNA library"
                        /tissue_type="bone marrow"
                        /cell_type="CD15+ myeloid progenitor cells"
                        /note="Organ: thymoid; Vector: pAMP10; mRNA made from thymoid carcinoma, cDNA made by oligo-dT priming. Non-directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 500 bp. Primary library. cDNA library Preparation: David B. Krizman, Ph.D. REFERENCE: Krizman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT      44 a       38 c       37 g       78 t
ORIGIN
Query Match           58.0%; Score 186.2; DB:12; Length 197;
Best Local Similarity 98.4%; Pred.NO.4.3e-37;
Matches 188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY   29 TTTGCTTTCCATATTACTATGTCTGTTCATTCACAAAACCSCCTTGACAGACACAG 88
     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   5  TTTTTTTTCCCATAATTACTATGTCTGTTCATTCACAAAACCSCCTTGACAGACACAG 64
QY   89 AAGTAGGAATTTGTTTGGAGAGAGGTGGCGCTGTGCAAATCGTTTCTTTTATATAGT 148
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   65 AAGTAGGAATTTGTTTGGAGAGAGGTGGCGCTGTGCAAATCGTTTCTTTTATATAGT 124
QY   149 TCTCAGTGCACATTCGCGGATTCCTGTATTTGTATTAATAATCCTTCCCTCCGCGG 208
     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   125 TCTCAGTGCACATTCGCGGATTCCTGTATTTGTATTAATAATCCTTCCCTCCGCGG 184
QY   209 TGGAAATACCA 219
     |||||||||
Db   185 TGGAAATACCA 195
RESULT 2
LOCUS      BQ228832                841 bp      mRNA      linear      EST 02-MAY-2002
DEFINITION AGENCOURT_7522585 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6051251
            5', mRNA sequence.
ACCESSION  BQ228832
VERSION    BQ228832.1 GI:20410232
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 841)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: rs9ab@rsfmail.nih.gov
            Tissue Procurement: ATCC/DCTP/DRP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.lnl.gov
            Plate: LLM13304 row: m column: 12
            High quality sequence stop: 87
            High quality sequence stop: 603.
            Location/Qualifiers
                1..841
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6051251"
FEATURES
    source          location/Qualifiers

```

[illegible]

/clone="3815552"  
 /clone\_lib="Sugano\_Kawakami\_zebrafish\_DRA"  
 /sex="mixed (one male and one female, including unfertilized eggs)"  
 /dev\_stage="adult"  
 /lib\_host="DH10B (phage resistant)"  
 /note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTC); Site 2: DraIII (CAACATGTC); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GTGGCTTACTG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTC, 3' site CACATGTC). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCTCTTAAGACTGCG and 3' end primer CGACCTGCAGCTCGACACA."  
 BASE COUNT 204 a 158 c 186 g 196 t  
 ORIGIN

Query Match 48.2%; Score 154.6; DB 12; Length 744;  
 Best Local Similarity 67.6%; Pred. No. 4.4e-29;  
 Matches 217; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1 GGTGTAAGTCTGCTGCTTCTCATCATGTTTCTCTATATTAATGTTCTGTTCC 60  
 DB 738 GGACTTACCCGGCTGGCTTCTCATCATGTTGCTCTACTCCAGCAATGTTTACTCC 679  
 QY 61 ATTCAAAAACCCCTTCGACAGCAGAGTAAGTAATGTTTGAAGAGAGTGCGT 120  
 DB 678 ATCTAATAGAGCGGATGACAGCAGAGCTGCGGGTGCAGCTGCAGAGACGCGGCC 619  
 QY 121 GTTGAATGCTTCTTCTTCTTCTGATGCTGATGCTGCTGCTGCTGCTGCTG 180  
 DB 618 ATGGACACCGCTTCTTCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 559  
 QY 181 GAGTAAATGCTTCTTCTTCTGCGGGTGAATACAGACATGATCTCTGATGATA 240  
 DB 558 ATGTCGAATATCTCTCTCTTAATGAGATGAGATACCAACCATCTCATCTTGGGTG 499  
 QY 241 GTGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 300  
 DB 498 GTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 439  
 QY 301 AACTTTTAAAGACAGTTG 321  
 DB 438 AGTTTTTCAAGACAGCTG 418

RESULT 4 ) 0 2 (b)

LOCUS AMA36170 235 bp mRNA linear EST 09-JUL-2000  
 DEFINITION 75600 MARC 2Pig Sus scrofa cDNA 5' mRNA sequence.  
 ACCESSION AMA36170  
 VERSION AMA36170.1 GI:6971476  
 KEYWORDS EST.

SOURCE  
 ORGANISM

Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 235)  
 Fahnenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,  
 Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.  
 and Keeler, J.W.  
 Design and use of two pooled tissue normalized cDNA libraries for  
 EST discovery in swine  
 Unpublished (2000)

TITLE  
 JOURNAL  
 COMMENT

Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366

Fax: 402 762 4390  
 Email: smitht@mail.marc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 20  
 and -minmatch 12 options.  
 PCR primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTCAAGCAG  
 Plate: 34 row: F column: 22  
 Seq primer: ATTTAGTGACACTATAG.  
 FEATURES  
 source  
 1..235  
 /organism="Sus scrofa"  
 /db\_xref="taxon:9823"  
 /clone\_lib="MARC 2Pig"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
 library made from pooled tissue from testis, ovary,  
 endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 49 a 64 c 45 g 77 t  
 ORIGIN

Query Match 47.4%; Score 152; DB 10; Length 235;  
 Best Local Similarity 87.0%; Pred. No. 2.1e-28;  
 Matches 167; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 130 CGTTCTTTTATATGCTTCTCTGATGCCATCTGCTGATTCCTGATTTAGTTAA 189  
 DB 5 CTTTCTTTTATATGAGGCTCTCTGATTCCTGATTCCTGATTCCTGATTTAGTTAA 64  
 QY 190 ATCTCTTCTCTCTGCGGGTGAATACAGACATGATCTCTGATTTAGTTAA 249  
 DB 65 ATTTCTCTCTCTCTGCGGGTGAATACAGACATGATCTCTGATTTAGTTAA 124  
 QY 250 TTCTCTCAGTTAAGAGTCTTTGAATCCATCTCTATCTGTCACCAACACTTTT 309  
 DB 125 TTCTCTCAGTTAAGAGTCTTTGAATCCATCTCTATCTGTCACCAACACTTTT 184  
 QY 310 AAGGACACTTG 321  
 DB 185 AAGGACACTTG 196

RESULT 5

LOCUS BF021857 456 bp mRNA linear EST 29-DEC-2000  
 DEFINITION uy58h08.y1 McCarrey Eddy round spermatid Mus musculus cDNA clone  
 IMAGE:3663807 5' similar to TR:09VYG0 G9VYG0 CG4187 PROTEIN. ;  
 mRNA sequence.

ACCESSION BF021857  
 VERSION BF021857.1 GI:10753189  
 KEYWORDS EST.

SOURCE  
 ORGANISM

Mus musculus  
 house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 456)  
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person  
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Rittler  
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterston, R. and Wilson, R.  
 The WashU-NCI Mouse EST Project 1999  
 Unpublished (1999)

TITLE  
 JOURNAL  
 COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.



**RESULT 7**

CNS016W/c LOCUS DEFINITION	CNS016W7  Drosophila melanogaster genome survey sequence T7 end of BAC BACN1C04 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	1100 bp  DNA  linear	GSS 26-JUL-1999
ACCSSION	AL107281		
VERSION	ALI07281.1	GI:5626586	
KEYWORDS	GSS.		
SOURCE	Drosophila melanogaster. Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridioidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 1 to 1100)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with The European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector PbeloBAC11.		
COMMENT			
FEATURES	Location/Qualifiers		
source	1..1100 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="BACN16C04" /clone_1lb="DrosBAC" /plasmid="PbeloBAC11" /note="end : 77"		
BASE COUNT	208 a 92 c 73 g 194 t 533 others		
ORIGIN			
Query Match	13.5%; Score 43.2; DB 17; Length 1100;		
Best Local Similarity	26.5%; Pred. No. 0.81;		
Matches	78; Conservative 87; Mismatches 129; Indels 0; Gaps 0;		
Oy	3 TGTCAGCTGCGTGGCTTCCATCATGTGTTGCCATATTACTAAGTGCTGCAT 62		
I:	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::		
Db	1053 TATSAMSTSMWSWBVBTSTWATSTMTASTATBTTSATVBWBSATWTTHBASINSYAT 994		
Oy	63 TCAAAAACCGCGCTTGCAGCACAGAAGTAAGCAATGTTTTGAACGAGCGTGGCT 122		
I:	:::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::		
Db	993 MYAAAASACAABMTAVAAAMTHASATAIVBASASVVSSAYTSCVSNAWCATMMKMT 934		
Oy	123 TGCAAATGCTTCTTTTATATAGTGTTCCTGCATGCCATTCGTCGATTCCTGATTTGT 182		
I:	: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::		
Db	933 TVTVVATSTCTTTFTTTHTTSHCTCBTTTTYTCTKTTCBPTCSMNTTYHWATCAIYYT 874		
Oy	183 AGTTAAATTCCTTCCTCCTCCGGGTGAATACACACATGATCTCCTGGTAGT 242		
I:	: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::		
Db	873 ATTTTMAAKAVARYRTCTMYSTSAXYAAYAATABMAABAABAMHMWAKRATTAT 814		
Oy	243 GATTTTTCCTTCACAGTTAACAGTCTTGAATCCATCCCTATFACTCTCAC 296		
I:	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::		
Db	813 GTSTAGMSTCKMGSTBCTBAMMKAKCYKBMBKCTAHKACACKBMSTVTXWRM 760		

**RESULT 8**

CNS04L3O LOCUS DEFINITION	CNS04L3O  Tetradodon nigroviridis genome survey sequence PUC-Ori end of clone 11D12 of library G from Tetraodon nigroviridis, genomic survey sequence.	992 bp  DNA  linear	GSS 21-MAY-2000
ACCSSION	AI295629		
VERSION	AI295629.1	GI:8034209	
KEYWORDS	GSS; genome survey sequence.		

SOURCE	ORGANISM
Tetraodon nigroviridis	Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;	
Tetraodontidae; Tetraodon.	
1 (bases 1 to 992)	
Roeest-Crollius,H., Jalllon,O., Dasiliva,C., Bouneau,L., Fisher,C., Bernot,A., Fizeses,C., Wincker,P., Brottler,P., Quetier,F., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.	
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	
Unpublished	
2 (bases 1 to 992)	
Roeest-Crollius,H., Jalllon,O., Dasiliva,C., Fizeses,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.	
freshwater pufferfish Tetraodon nigroviridis	
Unpublished	
3 (bases 1 to 992)	
Genoscope.	
Direct Submission	
Submitted (12-APR-2000)	
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon.	
Location/Qualifiers	
1..992	
/organism="Tetraodon nigroviridis"	
/db_xref="taxon:99883"	
/clone_1="17D12"	
/clone_1lb="G"	
/note="Genoscope sequence ID : COBG117DB06SP1-end ; PUC-Ori"	
BASE COUNT	241 a 150 c 104 g 406 t 91 others
ORIGIN	
Query Match	12.6%; Score 40.6; DB 17; Length 992;
Best Local Similarity	38.1%; Pred. No. 3.7;
Matches 109; Conservative 21; Mismatches 156; Indels 0; Gaps 0;	
Dn	22 CTCATCATGTGGTTTCCTAATTACTATAGTTCGTCATCAAAAACCGCCTTGACG 81 + :       - - - : :    : - : : - - - : : - - - : : - - - : 305 CKTATGCATAWTATWTTTATTTCCWCMTTCCCAAATWCYTCTACAAAGCGCGCACG 364 + : : : : : - - - : : - - - : : - - - : : - - - : : - - - : QY 82 ACCCAAGAAGTAAGGAATTTGTTGGAGAGAGAGGCGCTGCCAAATCGTTCTTTTT 141 + - - - - - : : - - - : : - - - : : - - - : : - - - : : - - - : Db 365 TCKTTTCCAAATYTKCNATTTTTCGGTAGATTTTCCCTTTTNTAATTTTTTTTTTTT 424 + - - - - - : : - - - : : - - - : : - - - : : - - - : : - - - : QY 142 ATAGTGTCTCGATGCGCATCTCGGAGATTCCTGATTTAGTAAATACCTTCCCTC 201 +           - - - : : - - - : : - - - : : - - - : : - - - : Db 425 TTTTITTTTATGTTTTTTTGGKTTCACATIGMTTTCGTAKTATACCATTTTTC 484 +           - - - : : - - - : : - - - : : - - - : : - - - : QY 202 TTCCGGGTGAANAACGACACAATGACTCTCGATAGTATGATTTTTTTTCCCTCCGACT 261 +           - - - : : - - - : : - - - : : - - - : : - - - : Db 485 TTYCAGKTKCTATTCACAACKTATTTTTCGCKRTTNNTNNTNNNTNNNNNNNTT 544 +           - - - : : - - - : : - - - : : - - - : : - - - : QY 262 AACAGTGTTCGAATCCCATCTCTATATCTGCACACCAACTTTT 307 ; +           - - - : : - - - : : - - - : : - - - : : - - - : Db 545 NNNNTTWTWTTCACAAAAATYCGTWTTCCTCCCAATTTAATWT 590 +           - - - : : - - - : : - - - : : - - - : : - - - :
RESULT 9	
LOCUS BH446416	660 bp DNA linear GSS 12-DEC-2001
DEFINITION BOHFUJ9TR BOHF Brassica oleracea genomic clone BOHFUJ9, DNA sequence.	
ACCESSION BH446416	
VERSION BH446416.1 GI:17632130	
KEYWORDS Brassica oleracea.	
SOURCE	





LOCUS	F.Rubripes GSS sequence, clone 0420505aa7, genomic survey sequence.
DEFINITION	FR020632 598 bp DNA linear GSS 10-DEC-1997
ACCESSION	AL013815
VERSION	AL013815.1 GI:2679883
KEYWORDS	GSS; genome survey sequence.
SOURCE	Takifugu rubripes.
ORGANISM	Takifugu rubripes
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
AUTHORS	Actinopterygii: Neopterygii: Teleostei: Euteleostei; Neoteleostei;
	Acanthomorpha: Acanthopterygii: Percomorpho: Tetraodontiformes;
	Tetraodontidae; Takifugu.
	1 (bases 1 to 598)
	Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y.,
	Williams,G. and Brenner,S.
TITLE	Direct Submission
JOURNAL	Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
	Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
COMMENT	Vector: pBluescript II KS
	V.type: phagemid
	PRIMER: KS
	DESCR:
	One pass dye-terminator sequencing of cosmid cloned genomic
	sequence.
FEATURES	location/Qualifiers
source	1..598
	/organism="Takifugu rubripes"
	/db_xref="taxon:31033"
	/clone="0420505aa7"
	/clone_11b="cosmid 0420505"
BASE COUNT	182 a 114 c 127 g 165 t 10 others
ORIGIN	
Query Match	11.8%; Score 37.6; DB 17; Length 598;
Best Local Similarity	53.4%; Pred. No. 19;
Matches	78; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
Oy	163 TCGCTGATTCGGTATTGTAGTTAAATCCCTTCCCTCCGGGTGGAATACCAGC 222
Db	350 TGCTAATAATTTTGAAATGCCCATTAACATGCACTTACAATCAAGGTTGCAAATACCACTT 291
Oy	223 ACAATGACTTCCGTGATAGTAGATTTTTTTCCTCCAGTTAACAGAGTCCTTGAATCCAATC 282
Db	290 AAAATTGGATGCACATATCATTTATTTCCCAAABACCAACCGTCGATTNTTATAGC 231
Oy	283 CTGTAFACTGCACACCACTTTT 308
Db	230 ATCTTTCTCTCCCAACCCCATTTT 205
RESULT 15	
CNSOL6CF	1201 bp DNA linear GSS 26-JUL-1999
LOCUS	Drosophila melanogaster genome survey sequence 17 end of BAC
DEFINITION	BACN15118 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL106569
VERSION	AL106569.1 GI:5622587
SOURCE	GSS.
KEYWORDS	Drosophila melanogaster.
ORGANISM	Drosophila melanogaster
	Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota;
	Neoptera: Endopterygota; Diptera: Brachycera; Muscomorpha;
	Ephyridroidea: Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 1201)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ;
	BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
	- Web : www.genoscope.cns.fr)
COMMENT	determination of this BAC-end sequence was carried out as part of a
	collaboration with the European Drosophila Genome Project (EDGP) -
	http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
	library (Dros BAC) was made by Alain Billaud at CEPH (Centre

d'Etude du polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES	Location/Qualifiers
source	1..1201 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="BACN15118" /clone_1ib="drosbac" /plasmid="pbeloBAC11" /note="end : T7"
BASE COUNT	235 a      265 c      159 g      325 t      217 others
ORIGIN	
Query Match	11.8%; Score 37.8; DB 17; Length 1201;
Best Local Similarity	34.5%; Pred. No. 19;
Matches 51; Conservative % 39; Mismatches 58; Indels 0; Gaps	
Oy 173 CTGATTTGTAGTAAATCCCTTCGCCCTCGGGTGGAATAACGACACATGACTT 2322	:   :   :   :   :   :           :   :   :   :   :
Dd 835 CTTBTYTTTKGBYTITTCASYTYGKCSIBSKKBNGTGCATITSKATWTIRRGGSST 894	K B Y I T T T C A S Y T Y G K C S I B S K K B N G T G C A I T S K A T W T I R R G G S S T
Oy 233 CGTGATAGTAGATTTTTTCTTCCTCAGTTAACAAGTGGCTTTGAATCAACCTCTAATAC 2922	: : : : :   : : : : :   : : : : :   : : : : :   : : : : :
Dd 895 TWKTDTKTTAAGNAATWNHNYHTVCTTYYHBCCTTSGSTTTWATATATACVTCTYTTY 9544	: : : : :   : : : : :   : : : : :   : : : : :   : : : : :
Oy 293 TCACAACAACACTTTTAAAGAACAAGTT 320	: : :       :   :   :   :
Dd 955 TAAAAAAMCTWTTTATTTATWGSCAAAAT 982	: : :       :   :   :   :

Search completed: May 26, 2003, 20:03:48  
Job time : 1753 secs

viii



GenCore version 5.1.4-p5\_4578  
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# OM protein - protein search, using sw model

Run on: May 22, 2003, 12:33:39 ; Search time 74 Seconds  
(without alignments)  
192.673 Million cell updates/sec

Title: US-09-930-312-2

Sequence: 1 GVMLLAFLIVFSTIMECS.....NSALNPILTYLTITNEFKDKL 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapect 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

A\_Geneseq\_101002:\*

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*

2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*

6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*

7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*

8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*

9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*

10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*

11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*

12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*

13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*

14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*

15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*

16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*

17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*

18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*

19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*

20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	549	100.0	107	23	AAE20148 Human novel G-prot
2	549	100.0	108	23	AAE20167 Human nGPCR-1079 v
3	549	100.0	109	23	AAE20168 Human nGPCR-1079 v
4	549	100.0	355	22	AAU04370 Human G-protein co
5	549	100.0	355	23	ABB06253 Human G-protein co
6	549	100.0	491	23	ABB06252 Human G-protein co
7	549	100.0	515	23	ABB06251 Human G-protein co
8	549	100.0	610	23	ABB06250 Human G-protein co
9	549	100.0	713	23	AAU97159 Human G-protein co
10	549	100.0	730	23	ABB06255 Human G-protein co

11	549	100.0	737	23	AAU97158 Human G-protein co
12	549	100.0	754	23	ABB06254 Human G-protein co
13	376	68.5	176	22	AAU87545 Human central nerv
14	376	68.5	176	22	AAU99972 Human expressed po
15	376	68.5	176	22	AAU99972 Human expressed po
16	376	68.5	176	22	ABB04062 Human musculoskele
17	376	68.5	176	22	ABB010249 Human CDNA SEQ ID
18	376	68.5	176	22	AAU8108 Human uterin
19	376	68.5	176	22	AAU8344 Human endocrine po
20	376	68.5	176	22	AAU18666 Human and cardiova
21	376	68.5	188	22	AAU21646 Human human neopla
22	376	68.5	209	22	AAU87243 Human expressed po
23	376	68.5	396	21	AAU57286 Human GPCR protein
24	376	68.5	722	20	AAU2171 Human CON222 G pro
25	376	68.5	757	20	AAU42170 Human LGR7 short f
26	376	68.5	757	20	AAU42170 Human LGR7 long fo
27	371	67.6	327	22	AAU80961 Human nGPCR57. Ho
28	370	67.4	140	21	AAU81526 Human OREX ORF1290
29	349	63.6	157	22	AAU35407 Human HGRL101 G-pr
30	234	42.6	334	22	AAU38929 Drosophila melanog
31	234	42.6	334	22	AAU38929 Drosophila G-prote
32	225	41.0	359	22	AAU8931 Drosophila melanog
33	225	41.0	359	22	AAU8931 Drosophila G-prote
34	210	38.3	1115	23	AAU7959 Lymnaea stagnalis
35	142.5	26.0	685	12	AAU11331 Human luteinising
36	142	25.9	861	22	AAU86961 Drosophila melanog
37	142	25.9	1300	22	AAU864083 Rat A3 adenosine r
38	138.5	25.2	320	16	AAU9450 N-terminal of LH r
39	136.5	24.9	361	14	AAU30406 N-terminal of LH r
40	136.5	24.9	386	14	AAU30500 N-terminal of LH r
41	136.5	24.9	638	14	AAU30499 N-terminal of LH r
42	136.5	24.9	692	14	AAU30503 N-terminal of LH r
43	136.5	24.9	693	14	AAU30510 N-terminal of LH r
44	136.5	24.9	698	14	AAU30505 N-terminal of LH r
45	136.5	24.9	699	14	AAU30517 N-terminal of LH r

## ALIGNMENTS

RESULT 1	AAE20148	AAE20148 standard; Protein: 107 AA.
ID	AAE20148	18-JUN-2002 (first entry)
AC	AAE20148	Human novel G-protein coupled receptor (nGPCR)-1079 protein.
DT	XX	Human: novel G-protein coupled receptor; nGPCR-1079; viral infection;
DT	XX	gene; therapy; human immunodeficiency virus; HIV; pain; migraine;
DT	XX	central nervous system disorder; stroke; manic depression; obesity;
DT	XX	metabolic disorder; anorexia; cardiovascular disorder; type 2 diabetes;
DT	XX	cancer; myocardial infarction; hypotension; degenerative disorder;
DT	XX	Parkinson's disease; Alzheimer's disease; neurological disorder;
DT	XX	schizophrenia; anxiety; inflammatory condition; rheumatoid arthritis;
DT	XX	thyroid disorder; autoimmune disorder; hormonal disorder; renal failure;
DT	XX	psoriasis; movement disorder; analgesic; cytoskeletal; neuroprotective;
DT	XX	anorectic; hypotensive; hypertensive; tranquilizer; anticonvulsant;
DT	XX	metabolic; neuroleptic; thrombolytic; cardiac; immunosuppressive.
DT	XX	Homo sapiens.
DT	XX	Key
DT	XX	Location/Qualifiers
DT	XX	4..26
DT	XX	/label= Transmembrane_domain
DT	XX	45..68
DT	XX	/label= Transmembrane_domain
DT	XX	77..99
DT	XX	/label= Transmembrane_domain
DT	XX	WO200214496-A2.

XX 21-FEB-2002.  
PD 15-AUG-2001; 2001WO-US25513.  
XX 15-AUG-2000; 2000US-225262P.  
XX (PHAA ) PHARMACIA & UPJOHN CO.  
XX Lind P;  
XX WPI; 2002-269192/31.  
XX An isolated nucleic acid molecule encoding novel G-protein coupled  
PT receptor polypeptide which is useful for treating obesity, diabetes,  
PT Parkinson's disease, manic depression, migraine, rheumatoid arthritis  
XX  
XX Claim 31; Page 60; 93pp; English.  
XX  
XX The patent discloses novel G-protein coupled receptor (ngPCR)-1079 genes  
CC and their corresponding proteins. Sequences of the invention are useful  
CC for treating diseases such as viral infections caused by human immuno-  
CC deficiency virus (HIV)-1 or 2, central nervous system (CNS) disorders  
CC (e.g. pain, including migraine, stroke, manic depression), metabolic  
CC disorders (e.g. obesity and anorexia), cancers, cardiovascular disorders  
CC (e.g. type 2 diabetes, myocardial infarction, hypotension), degenerative  
CC disorders (e.g. Parkinson's disease, Alzheimer's disease), neurological  
CC disorders (e.g. schizophrenia and anxiety), inflammatory conditions,  
CC rheumatoid arthritis, thyroid disorders, autoimmune disorders, hormonal  
CC disorders, renal failure, psoriasis and movement disorders. The present  
CC sequence is human ngPCR-1079 protein.  
XX  
SQ Sequence 107 AA:  
XX  
Query Match 100.0%; Score 549; DB 23; Length 107;  
Best Local Similarity 100.0%; Pred. No. 3.5e-66;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GVNLLAFLLIVFSYITMFCISIOKTALQTTTEVRNCFGEVAVANRFFIVPSDAICWIPVF 60  
DB 1 GVNLLAFLLIVFSYITMFCISIOKTALQTTTEVRNCFGEVAVANRFFIVPSDAICWIPVF 60  
QY 61 VVKILSLFRVEIPDPTMTSMWIVFFLPVNSALNPILYTLTTFNFKDKL 107  
DB 61 VVKILSLFRVEIPDPTMTSMWIVFFLPVNSALNPILYTLTTFNFKDKL 107  
XX  
RESULT 2  
AAE20167  
ID AAE20167 standard; Protein; 108 AA.  
XX  
AC AAE20167;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human ngPCR-1079 variant protein, Met-ngPCR-1079.  
XX  
XX Human; novel G-protein coupled receptor; ngPCR-1079; viral infection;  
KM gene; therapy: human immunodeficiency virus; HIV; pain; migraine;  
KM central nervous system disorder; stroke; manic depression; obesity;  
KM metabolic disorder; anorexia; cardiovascular disorder; type 2 diabetes;  
KM cancer; myocardial infarction; hypotension; degenerative disorder;  
KM Parkinson's disease; Alzheimer's disease; neurological disorder;  
KM schizophrenia; anxiety; inflammatory condition; rheumatoid arthritis;  
KM thyroid disorder; autoimmune disorder; hormonal disorder; renal failure;  
KM psoriasis; movement disorder; analgesic; cytoskeletal; neuroprotective;  
KM anorectic; hypotensive; hypertensive; tranquilizer; anticonvulsant;  
KM metabolic; neuroleptic; thrombolytic; cardiac; immunosuppressive;  
KM mutant; mutagen; variant.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX WO200214496-A2.  
XX 21-FEB-2002.  
XX 15-AUG-2001; 2001WO-US25513.  
XX 15-AUG-2000; 2000US-225262P.  
XX (PHAA ) PHARMACIA & UPJOHN CO.  
XX Lind P;  
XX WPI; 2002-269192/31.  
XX An isolated nucleic acid molecule encoding novel G-protein coupled  
PT receptor polypeptide which is useful for treating obesity, diabetes,  
PT Parkinson's disease, manic depression, migraine, rheumatoid arthritis  
XX  
XX Disclosure; Page -: 93pp; English.  
XX  
XX The patent discloses novel G-protein coupled receptor (ngPCR)-1079 genes  
CC and their corresponding proteins. Sequences of the invention are useful  
CC for treating diseases such as viral infections caused by human immuno-  
CC deficiency virus (HIV)-1 or 2, central nervous system (CNS) disorders  
CC (e.g. pain, including migraine, stroke, manic depression), metabolic  
CC disorders (e.g. obesity and anorexia), cancers, cardiovascular disorders  
CC (e.g. type 2 diabetes, myocardial infarction, hypotension), degenerative  
CC disorders (e.g. Parkinson's disease, Alzheimer's disease), neurological  
CC disorders (e.g. schizophrenia and anxiety), inflammatory conditions,  
CC rheumatoid arthritis, thyroid disorders, autoimmune disorders, hormonal  
CC disorders, renal failure, psoriasis and movement disorders. The present  
CC sequence is human ngPCR-1079 variant protein, Met-ngPCR-1079. This  
CC sequence is generated by the addition of a Met residue at position -1  
CC of human wild-type ngPCR-1079 protein.  
CC Note: This sequence is not shown in the specification but is derived from  
CC human wild-type ngPCR-1079 protein shown as SEQ ID NO: 2 in page 60 of  
CC the specification (AAE20148).  
XX  
SQ Sequence 108 AA:  
XX  
Query Match 100.0%; Score 549; DB 23; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.5e-66;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GVNLLAFLLIVFSYITMFCISIOKTALQTTTEVRNCFGEVAVANRFFIVPSDAICWIPVF 60  
DB 2 GVNLLAFLLIVFSYITMFCISIOKTALQTTTEVRNCFGEVAVANRFFIVPSDAICWIPVF 61  
QY 61 VVKILSLFRVEIPDPTMTSMWIVFFLPVNSALNPILYTLTTFNFKDKL 107  
DB 62 VVKILSLFRVEIPDPTMTSMWIVFFLPVNSALNPILYTLTTFNFKDKL 108  
XX  
RESULT 3  
AAE20168  
ID AAE20168 standard; Protein; 109 AA.  
XX  
AC AAE20168;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human ngPCR-1079 variant protein, Met-Lys-ngPCR-1079.  
XX  
XX Human; novel G-protein coupled receptor; ngPCR-1079; viral infection;  
KM gene; therapy: human immunodeficiency virus; HIV; pain; migraine;  
KM central nervous system disorder; stroke; manic depression; obesity;  
KM metabolic disorder; anorexia; cardiovascular disorder; type 2 diabetes;  
KM cancer; myocardial infarction; hypotension; degenerative disorder;  
KM Parkinson's disease; Alzheimer's disease; neurological disorder;  
KM schizophrenia; anxiety; inflammatory condition; rheumatoid arthritis;  
KM thyroid disorder; autoimmune disorder; hormonal disorder; renal failure;

KM psoriasis; movement disorder; analgesic; cytosolic; neuroprotective;  
 KM anorectic; hypotensive; hypertensive; tranquiliser; anticonvulsant;  
 KM metabolic; neuroleptic; thrombolytic; cardiant; immunosuppressive;  
 KM mutant; mutetin; variant.  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200214496-A2.  
 PD 21-FEB-2002.  
 XX 15-AUG-2001; 2001WO-US25513.  
 XX 15-AUG-2000; 2000US-225262P.  
 XX (PHMA ) PHARMACIA & UPJOHN CO.  
 PA Lind P;  
 PI WPI: 2002-269192/31.  
 DR An isolated nucleic acid molecule encoding novel G-protein coupled  
 PT receptor polypeptide which is useful for treating obesity, diabetes,  
 PT Parkinson's disease, manic depression, migraine, rheumatoid arthritis  
 PT  
 XX Disclosure; Page -: 93pp; English.  
 PS The patent discloses novel G-protein coupled receptor (GPCR)-1079 genes  
 XX and their corresponding proteins. Sequences of the invention are useful  
 CC for treating diseases such as viral infections caused by human immuno-  
 CC deficiency virus (HIV)-1 or 2, central nervous system (CNS) disorders  
 CC (e.g. pain, including migraine, stroke, manic depression), metabolic  
 CC disorders (e.g. obesity and anorexia), cancers, cardiovascular disorders  
 CC (e.g. type 2 diabetes, myocardial infarction, hypertension), degenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease), neurological  
 CC disorders (e.g. schizophrenia and anxiety), inflammatory conditions,  
 CC rheumatoid arthritis, thyroid disorders, autoimmune disorders, hormonal  
 CC disorders, renal failure, psoriasis and movement disorders. The present  
 CC sequence is human nGPCR-1079 variant protein, Met-Lys-nGPCR-1079. This  
 CC sequence is generated by the addition of Met-Lys residues at the amino  
 CC terminus (positions -2 and -1) of human wild-type nGPCR-1079 protein.  
 CC Note: This sequence is not shown in the specification but is derived from  
 CC human wild-type nGPCR-1079 protein, shown as SEQ ID NO: 2 in page 60 of  
 CC the specification (AAE20148).  
 CC  
 XX Sequence 109 AA:  
 SQ  
 Query Match 100.0%; Score 549; DB 23; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-66;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GVNLLAFILIVFSYITMCSIQKTAQTTEVRNCGREVAANRFFVFSDAICWIVF 60  
 DB 3 GVNLLAFILIVFSYITMCSIQKTAQTTEVRNCGREVAANRFFVFSDAICWIVF 62  
 QY 61 VKILSLFRVEIPDPTMTSMIVIFPLPVNSALNPILITLTTFEFDK 107  
 DB 63 VKILSLFRVEIPDPTMTSMIVIFPLPVNSALNPILITLTTFEFDK 109  
 RESULT 4  
 AAU04370  
 ID AAU04370 standard; Protein: 355 AA.  
 XX AAU04370;  
 AC 23-OCT-2001 (first entry)  
 DT Human G-protein coupled receptor, hRUP16.  
 XX Human G-protein coupled receptor; GPCR; hRUP16; agonist;  
 DE Human; G-protein coupled receptor; GPCR; hRUP16; agonist;  
 KW

KM Inverse agonist; Lung Cancer.  
 XX Homo sapiens.  
 OS WO200136471-A2.  
 PN 25-MAY-2001.  
 PD 16-NOV-2000; 2000WO-US31509.  
 PE 17-NOV-1999; 99US-0166088.  
 XX 17-NOV-1999; 99US-0166099.  
 PR 17-NOV-1999; 99US-0166369.  
 PR 23-DEC-1999; 99US-0171900.  
 PR 23-DEC-1999; 99US-0171901.  
 PR 23-DEC-1999; 99US-0171902.  
 PR 11-FEB-2000; 2000US-0181749.  
 PR 14-MAR-2000; 2000US-0189258.  
 PR 10-APR-2000; 2000US-0195898.  
 PR 10-APR-2000; 2000US-0195899.  
 PR 10-APR-2000; 2000US-0196078.  
 PR 28-APR-2000; 2000US-0200419.  
 PR 12-MAY-2000; 2000US-0203630.  
 PR 12-JUN-2000; 2000US-0210741.  
 PR 12-JUN-2000; 2000US-0210982.  
 PR 21-AUG-2000; 2000US-0226760.  
 PR 26-SEP-2000; 2000US-0235418.  
 PR 26-SEP-2000; 2000US-0235779.  
 PR 20-OCT-2000; 2000US-0242332.  
 PR 20-OCT-2000; 2000US-0242343.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 PI Chen R, Dang HT, Lowitz KP;  
 DR WPI: 2001-355616/37.  
 DR N-PSDB: AAS07943.  
 XX  
 PT Endogenous and non-endogenous versions of human G-protein coupled  
 PT receptors for direct identification of candidate compounds as agonists,  
 PT inverse agonists or partial agonists for use as therapeutic agents -  
 PS Claim 33; Page 105-106; 160pp; English.  
 XX  
 CC The sequence represents a human G-protein coupled receptor (GPCR),  
 CC hRUP16. The endogenous and non-endogenous, constitutively activated  
 CC versions of human G-protein coupled receptors (GPCR), are useful for  
 CC direct identification of candidate compounds as receptor agonists,  
 CC inverse agonists or partial agonists having applicability as therapeutic  
 CC agents for treating diseases related to GPCR, e.g. lung cancer.  
 CC Non-endogenous version of human GPCRs are also utilized in research  
 CC settings and in vitro and in vivo system, incorporating GPCRs can be  
 CC utilised to elucidate and understand the roles these receptors  
 CC play in the human condition, both normal and diseased.  
 CC  
 XX Sequence 355 AA:  
 SQ  
 Query Match 100.0%; Score 549; DB 22; Length 355;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-65;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GVNLLAFILIVFSYITMCSIQKTAQTTEVRNCGREVAANRFFVFSDAICWIVF 60  
 DB 197 GVNLLAFILIVFSYITMCSIQKTAQTTEVRNCGREVAANRFFVFSDAICWIVF 256  
 QY 61 VKILSLFRVEIPDPTMTSMIVIFPLPVNSALNPILITLTTFEFDK 107  
 DB 257 VKILSLFRVEIPDPTMTSMIVIFPLPVNSALNPILITLTTFEFDK 303  
 RESULT 5  
 ABB06253

ID ABB06253 standard; Protein: 355 AA.  
XX  
AC ABB06253;  
XX  
DT 23-MAY-2002 (first entry)  
XX  
DE Human G protein-coupled receptor TGR17-4 protein SEQ ID NO:10.  
XX  
KM Human; G protein-coupled receptor; TGR17-4; nootropic; antiinflammatory;  
KM vasotropic; immunomodulator; cytosolic; gene therapy; protein therapy;  
KM neurological; inflammatory; circulatory; degenerative; immune system;  
KM digestive disease; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200204640-A1.  
XX  
PD 17-JAN-2002.  
XX  
PF 06-JUL-2001; 2001WO-JP05878.  
XX  
PR 07-JUL-2000; 2000JP-0211989.  
XX  
PR 18-DEC-2000; 2000JP-0383794.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Moriya T, Ito T, Shintani Y, Miyajima N;  
XX  
DR WPI: 2002-179706/23.  
DR N-PSDB; ABL40194.  
XX  
PT G-protein coupled receptor protein TGR17 of human origin and DNA  
PT encoding it for diagnosis and treatment of cancer and circulatory and  
XX other diseases associated with its expression -  
XX  
PS Claim 1; Fig 8; 145pp; Japanese.  
XX  
CC The present invention describes a human guanine nucleotide binding  
CC protein (G protein) coupled receptor protein designated TGR17, which has  
CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
CC additional residues at the N-terminal. The TGR17 proteins have nootropic,  
CC antiinflammatory, vasotropic, immunomodulator and cytosolic activities.  
CC The TGR17 polynucleotides and protein can be used in gene therapy and  
CC protein therapy. G-protein coupled receptor proteins are cell membrane  
CC molecules mediating the cellular response to a large variety of signalling  
CC molecules. The TGR17 polynucleotides and proteins can be used in the  
CC diagnosis, treatment and prevention of diseases including neurological,  
CC inflammatory, circulatory, degenerative, immune system and digestive  
CC diseases and cancer. The present sequence represents human TGR17-4 from  
CC the present invention.  
XX  
SQ Sequence 355 AA:  
XX  
Query Match 100.0%; Score 549; DB:23; Length 355;  
Best Local Similarity 100.0%; Pred. No. 1.6e-65;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GVNLAFLLIVSYITMFCISIOKTALOTTEVRNCGREAVANRFFIVSDAICWIPVF 60  
DB 197 GVNLAFLLIVSYITMFCISIOKTALOTTEVRNCGREAVANRFFIVSDAICWIPVF 256  
XX  
QY 61 VVKILSFREIPDPTMTSMWIFFLPVNSALNPLLYLTNFFDKL 107  
DB 257 VVKILSFREIPDPTMTSMWIFFLPVNSALNPLLYLTNFFDKL 303  
XX  
RESULT 6  
ABB06252  
ID ABB06252 standard; Protein: 491 AA.  
XX  
AC ABB06252;  
XX  
DT 23-MAY-2002 (first entry)

XX  
DE Human G protein-coupled receptor TGR17-3 protein SEQ ID NO:7.  
XX  
KM Human; G protein-coupled receptor; TGR17-3; nootropic; antiinflammatory;  
KM vasotropic; immunomodulator; cytosolic; gene therapy; protein therapy;  
KM neurological; inflammatory; circulatory; degenerative; immune system;  
KM digestive disease; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200204640-A1.  
XX  
PD 17-JAN-2002.  
XX  
PF 06-JUL-2001; 2001WO-JP05878.  
XX  
PR 07-JUL-2000; 2000JP-0211989.  
XX  
PR 18-DEC-2000; 2000JP-0383794.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Moriya T, Ito T, Shintani Y, Miyajima N;  
XX  
DR WPI: 2002-179706/23.  
DR N-PSDB; ABL40192.  
XX  
PT G-protein coupled receptor protein TGR17 of human origin and DNA  
PT encoding it for diagnosis and treatment of cancer and circulatory and  
XX other diseases associated with its expression -  
XX  
PS Claim 3; Fig 7; 145pp; Japanese.  
XX  
CC The present invention describes a human guanine nucleotide binding  
CC protein (G protein) coupled receptor protein designated TGR17, which has  
CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
CC additional residues at the N-terminal. The TGR17 proteins have nootropic,  
CC antiinflammatory, vasotropic, immunomodulator and cytosolic activities.  
CC The TGR17 polynucleotides and protein can be used in gene therapy and  
CC protein therapy. G-protein coupled receptor proteins are cell membrane  
CC molecules mediating the cellular response to a large variety of signalling  
CC molecules. The TGR17 polynucleotides and proteins can be used in the  
CC diagnosis, treatment and prevention of diseases including neurological,  
CC inflammatory, circulatory, degenerative, immune system and digestive  
CC diseases and cancer. The present sequence represents human TGR17-3 from  
CC the present invention.  
XX  
SQ Sequence 491 AA:  
XX  
Query Match 100.0%; Score 549; DB:23; Length 491;  
Best Local Similarity 100.0%; Pred. No. 2.5e-65;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GVNLAFLLIVSYITMFCISIOKTALOTTEVRNCGREAVANRFFIVSDAICWIPVF 60  
DB 333 GVNLAFLLIVSYITMFCISIOKTALOTTEVRNCGREAVANRFFIVSDAICWIPVF 392  
XX  
QY 61 VVKILSFREIPDPTMTSMWIFFLPVNSALNPLLYLTNFFDKL 107  
DB 393 VVKILSFREIPDPTMTSMWIFFLPVNSALNPLLYLTNFFDKL 439  
XX  
RESULT 7  
ABB06251  
ID ABB06251 standard; Protein: 515 AA.  
XX  
AC ABB06251;  
XX  
DT 23-MAY-2002 (first entry)  
XX  
DE Human G protein-coupled receptor TGR17-2 protein SEQ ID NO:5.  
XX  
KM Human; G protein-coupled receptor; TGR17-2; nootropic; antiinflammatory;  
KM vasotropic; immunomodulator; cytosolic; gene therapy; protein therapy;

KW neurological; inflammatory; circulatory; degenerative; immune system;  
 KW digestive disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200204640-A1.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 06-JUL-2001; 2001WO-JP05878.  
 XX  
 PR 07-JUL-2000; 2000JP-0211989.  
 PR 18-DEC-2000; 2000JP-0383794.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Moriya T, Ito T, Shintani Y, Miyajima N;  
 DR WPI: 2002-179706/23.  
 DR N-PSDB: ABL40191.  
 XX  
 PT G-protein coupled receptor protein TGR17 of human origin and DNA  
 PT encoding it for diagnosis and treatment of cancer and circulatory and  
 PT other diseases associated with its expression -  
 XX  
 PS Claim 3; Fig 6; 145pp; Japanese.  
 CC The present invention describes a human guanine nucleotide binding  
 CC protein (G protein) coupled receptor protein designated TGR17, which has  
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
 CC additional residues at the N-terminal. The TGR17 proteins have nootropic,  
 CC antiinflammatory, vasotropic, immunomodulator and cyostatic activities.  
 CC The TGR17 polynucleotides and protein can be used in gene therapy and  
 CC protein therapy. G-protein coupled receptor proteins are cell membrane  
 CC proteins mediating the cellular response to a large variety of signalling  
 CC molecules. The TGR17 polynucleotides and proteins can be used in the  
 CC diagnosis, treatment and prevention of diseases including neurological,  
 CC inflammatory, circulatory, degenerative, immune system and digestive  
 CC diseases and cancer. The present sequence represents human TGR17-2 from  
 CC the present invention.  
 CC  
 SQ Sequence 515 AA;  
 Query Match 100.0%; Score 549; DB 23; Length 515;  
 Best Local Similarity 100.0%; Pred. No. 2,6e-65;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GVNLLAFLLIVFSYITMFCSTQKTALQTEVRNCFGRVAVANRRFFVFSDAICWIPVF 60  
 DB 357 GVNLLAFLLIVFSYITMFCSTQKTALQTEVRNCFGRVAVANRRFFVFSDAICWIPVF 416  
 QY 61 VKILSLFRVEIPDPTMSWIVIFFLPVNSALNPILYTLTTFNFFDKL 107  
 DB 417 VKILSLFRVEIPDPTMSWIVIFFLPVNSALNPILYTLTTFNFFDKL 463  
 RESULT 8  
 ABB06250  
 ID ABB06250 standard; Protein: 610 AA.  
 XX  
 AC ABB06250;  
 XX  
 DT 23-MAY-2002 (first entry)  
 XX  
 DE Human G protein-coupled receptor TGR17-1 protein SEQ ID NO.1.  
 XX  
 KW Human; G protein-coupled receptor; TGR17-1; nootropic; antiinflammatory;  
 KW vasotropic; immunomodulator; cyostatic; gene therapy; protein therapy;  
 KW neurological; inflammatory; circulatory; degenerative; immune system;  
 KW digestive disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX

PN WO200204640-A1.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 06-JUL-2001; 2001WO-JP05878.  
 XX  
 PR 07-JUL-2000; 2000JP-0211989.  
 PR 18-DEC-2000; 2000JP-0383794.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Moriya T, Ito T, Shintani Y, Miyajima N;  
 DR WPI: 2002-179706/23.  
 DR N-PSDB: ABL40188.  
 XX  
 PT G-protein coupled receptor protein TGR17 of human origin and DNA  
 PT encoding it for diagnosis and treatment of cancer and circulatory and  
 PT other diseases associated with its expression -  
 XX  
 PS Claim 3; Fig 5; 145pp; Japanese.  
 CC The present invention describes a human guanine nucleotide binding  
 CC protein (G protein) coupled receptor protein designated TGR17, which has  
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
 CC additional residues at the N-terminal. The TGR17 proteins have nootropic,  
 CC antiinflammatory, vasotropic, immunomodulator and cyostatic activities.  
 CC The TGR17 polynucleotides and protein can be used in gene therapy and  
 CC protein therapy. G-protein coupled receptor proteins are cell membrane  
 CC proteins mediating the cellular response to a large variety of signalling  
 CC molecules. The TGR17 polynucleotides and proteins can be used in the  
 CC diagnosis, treatment and prevention of diseases including neurological,  
 CC inflammatory, circulatory, degenerative, immune system and digestive  
 CC diseases and cancer. The present sequence represents human TGR17-1 from  
 CC the present invention.  
 CC  
 SQ Sequence 610 AA;  
 Query Match 100.0%; Score 549; DB 23; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 3,2e-65;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GVNLLAFLLIVFSYITMFCSTQKTALQTEVRNCFGRVAVANRRFFVFSDAICWIPVF 60  
 DB 452 GVNLLAFLLIVFSYITMFCSTQKTALQTEVRNCFGRVAVANRRFFVFSDAICWIPVF 511  
 QY 61 VKILSLFRVEIPDPTMSWIVIFFLPVNSALNPILYTLTTFNFFDKL 107  
 DB 512 VKILSLFRVEIPDPTMSWIVIFFLPVNSALNPILYTLTTFNFFDKL 558  
 RESULT 9  
 AAU97159  
 ID AAU97159 standard; Protein: 713 AA.  
 XX  
 AC AAU97159;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Human G-protein coupled receptor HGPBMY5 splice variant.  
 XX  
 KW Human; G-protein coupled receptor; GPCR; HGPBMY5; colon; brain;  
 KW ovary; thymus; lung; immune system; cancer; immune disorder;  
 KW neurological disorder; infection; human immunodeficiency virus; HIV;  
 KW antiinfect; antiasthmatic; dermatological; antiarteriosclerotic;  
 KW antidiabetic; nephrotropic; osteopathic; antiarthritic;  
 KW antiinflammatory; antirheumatic; antithyroid; cyostatic; vulnerary;  
 KW virucide; antibacterial; antifungal; antiparasitic; protozoacide;  
 KW antihelminthic; nootropic; neuroprotective; antidepressant;  
 KW anticonvulsant; antiparkinsonian; neuroleptic; anti-HIV; receptor.  
 XX  
 OS Homo sapiens.  
 XX

PN WO200226824-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 26-SEP-2001: 2001WO-US30365.  
 XX  
 PR 27-SEP-2000: 2000US-235713P.  
 XX 16-JAN-2001: 2001US-261781P.  
 PR 19-JUL-2001: 2001US-306605P.  
 PR 03-AUG-2001: 2001US-310436P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Feder JN, Mintier G, Ramanathan CS, Hawken DR:  
 DR WPI: 2002-435196/46.  
 DR N-PSDB; ABR51947.  
 XX  
 PT Novel G protein-coupled receptor, HGRBM5 polypeptide, useful for  
 PT treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative  
 PT colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,  
 PT osteoarthritis  
 XX  
 PS Claim 11: Fig 6: 148bp: English.  
 XX  
 CC The present invention relates to the isolation of a novel human  
 CC G-protein coupled receptor (GPCR) (HGRBM5), and the polynucleotide  
 CC sequence encoding it. The HGRBM5 polypeptide and polynucleotide  
 CC are useful for preventing, treating or ameliorating a disease.  
 CC disorder or condition related to the colon, brain, ovaries, thymus,  
 CC lungs or immune system. They are particularly useful for the  
 CC treatment or prevention of cancers, immune disorders, neurological  
 CC disorders, and diseases related to the brain, ovaries, thymus or  
 CC lungs. The polynucleotide sequence is useful for diagnosing or  
 CC determining susceptibility to infections such as bacterial, fungal,  
 CC protozoan and viral infections, particularly infections caused by  
 CC human immunodeficiency virus (HIV or HIV-2). The present sequence  
 CC represents a splice variant of human GPCR HGRBM5.  
 XX  
 SQ Sequence 713 AA:  
 Query Match 100.0%; Score 549; DB 23; Length 713;  
 Best Local Similarity 100.0%; Pred. No. 4e-65;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GVNLALFLIVFSYITMFCSIQKTALQTEVRNCFGREAVANRFFIVSDAICWIPVF 60  
 DB 555 GVNLALFLIVFSYITMFCSIQKTALQTEVRNCFGREAVANRFFIVSDAICWIPVF 614  
 QY 61 VVILSLFRVEIPDPTMTSWIVIFFLPVNSALNPILYLTITNFEKDKL 107  
 DB 615 VVILSLFRVEIPDPTMTSWIVIFFLPVNSALNPILYLTITNFEKDKL 661  
 RESULT 10  
 ABB06255  
 ID ABB06255 standard; Protein: 730 AA.  
 XX  
 AC ABB06255;  
 XX  
 DT 23-MAY-2002 (first entry)  
 XX  
 DE Human G protein-coupled receptor TGR17-6 protein SEQ ID NO:15.  
 XX  
 KW Human; G protein-coupled receptor; TGR17-6; nocotropic; antiinflammatory;  
 KW vasotropic; immunomodulator; cytostatic; gene therapy; protein therapy;  
 KW neurological; inflammatory; circulatory; degenerative; immune system;  
 KW digestive disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200204640-A1.  
 XX

PD 17-JAN-2002.  
 XX  
 PF 06-JUL-2001: 2001WO-JP05878.  
 XX  
 PR 07-JUL-2000: 2000JP-0211989.  
 PR 18-DEC-2000: 2000JP-0383794.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Moriya T, Ito T, Shintani Y, Miyajima N;  
 DR WPI: 2002-179706/23.  
 DR N-PSDB; ABL40197.  
 XX  
 PT G-protein coupled receptor protein TGR17 of human origin and DNA  
 PT encoding it for diagnosis and treatment of cancer and circulatory and  
 PT other diseases associated with its expression  
 XX  
 PS Claim 3: Fig 12: 145bp: Japanese.  
 XX  
 CC The present invention describes a human guanine nucleotide binding  
 CC protein (G protein) coupled receptor protein designated TGR17, which has  
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
 CC additional residues at the N-terminal. The TGR17 proteins have nocotropic,  
 CC antiinflammatory, vasotropic, immunomodulator and cytostatic activities.  
 CC The TGR17 polynucleotides and protein can be used in gene therapy and  
 CC protein therapy. G-protein coupled receptor proteins are cell membrane  
 CC proteins mediating the cellular response to a large variety of signalling  
 CC molecules. The TGR17 polynucleotides and proteins can be used in the  
 CC diagnosis, treatment and prevention of diseases including neurological,  
 CC inflammatory, circulatory, degenerative, immune system and digestive  
 CC diseases and cancer. The present sequence represents human TGR17-6 from  
 CC the present invention.  
 XX  
 SQ Sequence 730 AA:  
 Query Match 100.0%; Score 549; DB 23; Length 730;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-65;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GVNLALFLIVFSYITMFCSIQKTALQTEVRNCFGREAVANRFFIVSDAICWIPVF 60  
 DB 572 GVNLALFLIVFSYITMFCSIQKTALQTEVRNCFGREAVANRFFIVSDAICWIPVF 631  
 QY 61 VVILSLFRVEIPDPTMTSWIVIFFLPVNSALNPILYLTITNFEKDKL 107  
 DB 632 VVILSLFRVEIPDPTMTSWIVIFFLPVNSALNPILYLTITNFEKDKL 678  
 RESULT 11  
 AAU97158  
 ID AAU97158 standard; Protein: 737 AA.  
 XX  
 AC AAU97158;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Human G-protein coupled receptor HGRBM5.  
 XX  
 KW Human; G-protein coupled receptor; GPCR; HGRBM5; colon; brain;  
 KW ovary; thymus; lung; immune system; cancer; immune disorder;  
 KW neurological disorder; infection; human immunodeficiency virus; HIV;  
 KW antiallergic; antidiabetic; dermatological; antiatherosclerotic;  
 KW antitumor; antidiabetic; nephrotropic; osteopathic; antiarthritic;  
 KW antiinflammatory; antirheumatic; antithyroid; cytostatic; vulnerary;  
 KW virucide; antibacterial; antifungal; antiparasitic; protozoacide;  
 KW antihelmintic; nocotropic; neuroprotective; antidepressant;  
 KW anticonvulsant; antiparkinsonian; neuroleptic; anti-HIV; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200226824-A2.  
 XX

PD 04-APR-2002.  
 XX  
 XX 26-SEP-2001; 2001WO-US30365.  
 XX  
 XX 27-SEP-2000; 2000US-235713P.  
 PR 16-JAN-2001; 2001US-261781P.  
 PR 19-JUL-2001; 2001US-30605P.  
 PR 03-AUG-2001; 2001US-310436P.  
 XX  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO;  
 XX  
 XX Feder JN, Mintler G, Ramanathan CS, Hawken DR;  
 DR WPI: 2002-435196/46.  
 DR N-PSDB: ABK51944.  
 XX  
 PT Novel G protein-coupled receptor, HGPRBM5 polypeptide, useful for  
 PT treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative  
 PT colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,  
 PT osteoarthritis -  
 XX  
 PS Claim 11; Fig 2; 148pp: English.  
 XX  
 CC The present invention relates to the isolation of a novel human  
 CC G-protein coupled receptor (GPCR) (HGPRBM5), and the polynucleotide  
 CC sequence encoding it. The HGPRBM5 polypeptide and polynucleotide  
 CC are useful for preventing, treating or ameliorating a disease,  
 CC disorder or condition related to the colon, brain, ovaries, thymus,  
 CC lungs or immune system. They are particularly useful for the  
 CC treatment or prevention of cancers, immune disorders, neurological  
 CC disorders, and diseases related to the brain, ovaries, thymus or  
 CC lungs. The polynucleotide sequence is useful for diagnosing or  
 CC determining susceptibility to infections such as bacterial, fungal,  
 CC protozoan and viral infections, particularly infections caused by  
 CC human immunodeficiency virus (HIV or HIV-2). The present sequence  
 CC represents human GPCR HGPRBM5.  
 CC  
 XX  
 SQ Sequence 737 AA;  
 Query Match 100.0%; Score 549; DB 23; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-65;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GVNLLAFLLIYFSYITMFCSTQKATLOTTEVRNCGREVAANRFFVFESDAICWIPVF 60  
 DB 579 GVNLLAFLLIYFSYITMFCSTQKATLOTTEVRNCGREVAANRFFVFESDAICWIPVF 638  
 QY 61 VKILSLFRVEIPDTMTSMIVIFFLPVNSALNPILYTLTTFNFKDKL 107  
 DB 639 VKILSLFRVEIPDTMTSMIVIFFLPVNSALNPILYTLTTFNFKDKL 685  
 RESULT 12  
 ABB06254  
 ID ABB06254 standard; Protein: 754 AA.  
 XX  
 AC ABB06254;  
 XX  
 DT 23-MAY-2002 (first entry)  
 XX  
 DE Human G protein-coupled receptor TGR17-5 protein SEQ ID NO:13.  
 XX  
 KW Human: G protein-coupled receptor; TGR17-5; nocotropic; antiinflammatory;  
 KW vasotropic; immunomodulator; cyostatic; gene therapy; protein therapy;  
 KW neurological; inflammatory; circulatory; degenerative; immune system;  
 KW digestive disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W0200204640-A1.  
 XX  
 PD 17-JAN-2002.  
 XX

PF 06-JUL-2001; 2001WO-JP05878.  
 XX  
 XX 07-JUL-2000; 2000JP-0211989.  
 PR 18-DEC-2000; 2000JP-0383794.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA  
 PI Moriya T, Ito T, Shuntani Y, Miyajima N;  
 DR WPI: 2002-179706/23.  
 DR N-PSDB: ABL40196.  
 XX  
 PT G-protein coupled receptor protein TGR17 of human origin and DNA  
 PT encoding it for diagnosis and treatment of cancer and circulatory and  
 PT other diseases associated with its expression -  
 XX  
 PS Claim 3; Fig 11; 145pp: Japanese.  
 XX  
 CC The present invention describes a human guanine nucleotide binding  
 CC protein (G protein) coupled receptor protein designated TGR17, which has  
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
 CC additional residues at the N-terminal. The TGR17 proteins have nocotropic,  
 CC antiinflammatory, vasotropic, immunomodulator and cyostatic activities.  
 CC The TGR17 polynucleotides and protein can be used in gene therapy and  
 CC protein therapy. G-protein coupled receptor proteins are cell membrane  
 CC proteins mediating the cellular response to a large variety of signalling  
 CC molecules. The TGR17 polynucleotides and proteins can be used in the  
 CC diagnosis, treatment and prevention of diseases including neurological,  
 CC inflammatory, circulatory, degenerative, immune system and digestive  
 CC diseases and cancer. The present sequence represents human TGR17-5 from  
 CC the present invention.  
 CC  
 XX  
 SQ Sequence 754 AA;  
 Query Match 100.0%; Score 549; DB 23; Length 754;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-65;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GVNLLAFLLIYFSYITMFCSTQKATLOTTEVRNCGREVAANRFFVFESDAICWIPVF 60  
 DB 596 GVNLLAFLLIYFSYITMFCSTQKATLOTTEVRNCGREVAANRFFVFESDAICWIPVF 655  
 QY 61 VKILSLFRVEIPDTMTSMIVIFFLPVNSALNPILYTLTTFNFKDKL 107  
 DB 656 VKILSLFRVEIPDTMTSMIVIFFLPVNSALNPILYTLTTFNFKDKL 702  
 RESULT 13  
 AAU87545  
 ID AAU87545 standard; Protein: 176 AA.  
 XX  
 AC AAU87545;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE Novel central nervous system protein #455.  
 XX  
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;  
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
 KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;  
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
 KW myocardial infarction; wound healing; cell proliferation; skin aging;  
 KW food additive; food preservative; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W0200155318-A2.  
 XX  
 PD 02-AUG-2001.  
 XX





XX New isolated nucleic acid encoding a protein for diagnosing,  
PT preventing, treating or ameliorating medical conditions and used as  
PT food additives or preservatives -  
XX  
XX  
PS Claim 9; SEQ ID No 1063; 837bp; English.  
XX  
CC The invention describes an isolated nucleic acid molecule (I) encoding a  
CC novel central nervous system protein (I) and polypeptides (II) encoded  
CC by (I), are used to treat a medical conditions and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardial  
CC infection. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,  
CC  
Query Match 68.5%; Score 376; DB 22; Length 176;  
Best Local Similarity 64.5%; Pred. No. 1,6e-42;  
Matches 69; Conservative 20; Mismatches 18; Indels 0; Gaps 0;  
QY 1 GVNLAFLIIVSYITMFCSTOKTALQTEVENCGRVAVANREFEIVSDAICWIFVF 60  
Db 11 GINLAFLIIVSYSGSMFYSVHOSAITATEIRNOVKKEMIAKRFFEIFDLCWIDIF 70  
QY 61 VKKILSLRVEIPDPTMTSMIVIFFLPVNSALNPILYTLTTFEKKKL 107  
Db 71 VKKILSLQVEIPGTTTSMVVFILPINSALNPILYTLTTRPEKMT 117  
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ID AAM99972 standard; Protein: 176 AA.  
XX AAM99972;  
AC  
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XX  
DT 04-JAN-2002 (first entry)  
XX  
XX  
DE Human expressed polypeptide SEQ ID NO 96.  
XX  
XX  
XX Human; nontropic; neuroprotective; cytosolic; dermatological; virocidic;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;  
KW antipneumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antidiabetic; antidiabetic; antidiabetic; anticonvulsant; antifungal;  
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200155387-A1.  
XX  
XX 02-AUG-2001.  
PD  
XX  
PF 17-JAN-2001; 2001WO-US01310.  
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PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
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PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.

PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 20-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
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PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
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PR 08-NOV-2000; 2000US-0246610.  
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PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0251988.  
PR 06-DEC-2000; 2000US-0251479.  
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PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX  
DR WPI: 2001-46573/50.  
DR N-PSDB; AA199584.  
XX  
XX  
PT Isolated digestive system associated polypeptide for treating,  
PT preventing and/ or prognosing disorders related to the digestive system  
PT including digestive system cancers and also for testing and detection  
e.g. diagnosis -  
XX

PS Claim 11; SEQ ID NO 96; 509pp + Sequence Listing; English.  
XX  
CC The invention relates to novel genes (AA199548-AA199604) and proteins  
CC (AAM99936-AAM99984) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 176 AA:  
Query Match 68.5%; Score 376; DB 22; Length 176;  
Best Local Similarity 64.5%; Pred. No. 1,6e-42;  
Matches 69; Conservative 20; Mismatches 18; Indels 0; Gaps 0;  
QY 1 GVNLAFLIIVFSYITMFCSTOKALOTTEVRNCFGRVAVANRFFIVSDAICWIPVF 60  
Db 11 GINLAFLIIVFSYSGMFYSVHOSAITATEIRNOVKREMIARFFIVFTDALCWIPIF 70  
QY 61 VKILSLFRVEIPDTMTSMWIVFPLPVNSALNPILYLTITNFFKDKL 107  
Db 71 VKFLSLQVEIRPCTITSMWVIFILPINSALNPILYLTITNFFKDKL 117  
RESULT 15  
ID ABB04062 standard; Protein: 176 AA.  
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XX ABB04062:  
AC 08-JAN-2002 (first entry)  
DT  
XX  
XX Human musculoskeletal system related polypeptide SEQ ID NO 2009.  
DE  
XX  
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
KW vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein;  
KW musculoskeletal system.  
XX  
OS Homo sapiens.  
PN WO200155367-A1.  
XX  
XX  
XX 02-AUG-2001.  
PD  
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XX 17-JAN-2001; 2001WO-US01338.  
PF  
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XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
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PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
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PR 18-APR-2000; 2000US-0198123.  
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PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.



CC other cancers of the adrenal gland, bone, bone marrow, breast,  
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
 CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound  
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;  
 CC and (f) infectious diseases such as viral, bacterial, fungal and  
 CC parasitic infections.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX

SQ Sequence 176 AA:

Query Match 68.5%; Score 376; DB 22; Length 176;

Best Local Similarity 64.5%; Pred. No. 1.6e-42; Mismatches 18; Indels 0; Gaps 0;

Matches 69; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

QY 1 GVNLLAEFLIVFSYITMFCSIQKTAIQTEVRNCGREAVANRFFIVFSDAICWIPVF 60

Db 11 GINLAAPLIIIVFSYSGSMFYSVHOSAITATEIRNQVKKEMILAKRFFIVFTDALCWIPF 70

QY 61 VVKILSLFREIDPTMTSMVIFELPNYSALNPILTYLTITNFFKDKL 107

Db 71 VVKFLSLQVEIPGTITSMVIFELPNYSALNPILTYLTITTRPERKMT 117

Search completed: May 22, 2003, 12:45:00  
 Job time : 76 secs

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: May 22, 2003, 12:43:45 ; Search time 29 Seconds  
(without alignments)  
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Title: US-09-930-312-2

Perfect score: 549

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Scoring table:

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	139.5	25.4	696	4	US-07-757-342D-4
3	138.5	25.2	320	1	US-08-101-435-4
4	138.5	25.2	611	4	US-07-757-342D-8
5	138.5	25.2	636	4	US-07-757-342D-7
6	138.5	25.2	674	4	US-07-757-342D-10
7	138.5	25.2	699	4	US-07-757-342D-2
8	136.5	24.9	700	4	US-07-757-342D-3
9	129.5	23.6	795	4	US-07-741-453A-55
10	127.5	23.2	332	5	US-08-118-270-53
11	127.5	23.2	332	5	PCT-US93-08528-53
12	125	22.8	420	4	US-08-795-876-33
13	125	22.8	423	4	US-08-795-876-38
14	125	22.8	436	4	US-08-795-876-2
15	125	22.8	695	3	US-08-487-886-2
16	125	22.8	695	3	US-08-482-855-2
17	125	22.8	695	3	US-08-474-986-2
18	123	22.4	194	1	US-07-918-314-4
19	123	22.4	326	1	US-07-918-314-6
20	123	22.4	326	1	US-08-349-696-19
21	123	22.4	326	1	US-08-233-009-19
22	123	22.4	326	2	US-08-560-231-19
23	123	22.4	326	4	US-09-080-704A-19
24	122.5	22.3	764	4	US-07-741-453A-60
25	122	22.2	692	4	US-07-757-342D-6
26	120.5	21.9	764	4	US-07-741-453A-54
27	120	21.9	326	1	US-08-293-563-7

28	119.5	21.8	318	1	US-08-349-696-25	Sequence 25, Appl
29	119.5	21.8	318	1	US-08-233-009-25	Sequence 25, Appl
30	119.5	21.8	318	2	US-08-560-231-25	Sequence 25, Appl
31	119.5	21.8	318	4	US-09-080-704A-25	Sequence 25, Appl
32	119.5	21.8	336	1	US-08-118-270-54	Sequence 54, Appl
33	119.5	21.8	336	5	PCT-US93-08528-54	Sequence 54, Appl
34	119.5	21.8	764	4	US-07-741-453A-59	Sequence 59, Appl
35	119.5	21.8	764	4	US-07-741-453A-61	Sequence 61, Appl
36	118.5	21.6	764	4	US-07-757-342D-5	Sequence 5, Appl
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39	115	20.9	332	2	US-08-560-231-23	Sequence 23, Appl
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41	113.5	20.7	334	1	US-08-118-270-73	Sequence 73, Appl
42	113.5	20.7	334	5	PCT-US93-08528-73	Sequence 73, Appl
43	110	20.0	332	1	US-08-233-009-23	Sequence 23, Appl
44	109	19.9	644	2	US-08-866-757-2	Sequence 2, Appl
45	109	19.9	644	4	US-09-153-593-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-07-741-453A-56  
Sequence 56, Application US/07741453A  
Patent No. 6228597  
GENERAL INFORMATION:  
APPLICANT: PARMENTIER, MARC  
APPLICANT: LIBERT, FREDERIC  
APPLICANT: DOMONT, JACQUES  
APPLICANT: VASSART, GILBERT  
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
STREET: 1615 L STREET, N.W.  
CITY: WASHINGTON, D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/741,453A  
FILING DATE: 19911015  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16773  
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 792 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-741-453A-56  
Query Match 26.0%; Score 142.5; DB 4; Length 792;  
Best Local Similarity 27.9%; Pred. No. 4,5e-08;  
Matches 31; Conservative 24; Mismatches 43; Indels 13; Gaps 2;  
QY 1 GVNLAFLLIVFSYITMFCSSIQKALQTEVRNCGEVAVARPFFIYSDAICMIPVF 60

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QY      61  V K I I S L E R V E ----- I P D T M T S W I V I E P L P V N S A L N P I L X T L T N F K R    104
Db      665 H C G P I S F E A I S A L K V P L I T Y T N S K V L L V E F Y P V N S C A N P F L V I A F T K A P R    715
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RESULT 2  
US-07-757-342D-4

Sequence 4, Application US/07757342D,  
Patent No. 6318509

GENERAL INFORMATION:

APPLICANT: IGARASHI, Masao  
MINEGISHI, Takashi  
NAKAMURA, Kazuto

CORRESPONDENCE ADDRESS:

STREET: 130 Water Street

COMPUTER READABLE FORM:

SEQUENCE	DESCRIPTION:	SEQ ID NO:	4:
US-07-757-342D-4			

RESULT 3  
US-08-101-435-4

; Sequence 4, Application US/08101435

GENERAL INFORMATION:

NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allgretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 300C  
CITY: Chicago  
STATE: IL  
COUNTRY: USA

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
;

```

MOLECULE T  
US-08-101-435-4

RESULT 4  
US-07-757-342D-8

```

; GENERAL INFORMATION:
;
; APPLICANT: IGARASHI, Masao

```

STREET: 130 Water Street

```

?      COMPUTER READABLE FORM:
?
?      MEDIUM TYPE: floppy disk
?
?      COMPUTER: IBM PC compatible
?
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?
?      SOFTWARE: PatentIn Release #1.0, Version #1.25
?
?      CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/07/757,342D  
FILING DATE: 10-Sep-1991  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BUCKLEY, Linda M.  
REGISTRATION NUMBER: 31003  
REFERENCE/DOCKET NUMBER: 41226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 611 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-07-757-342D-8

Query Match 25.2%; Score 138.5; DB 4; Length 611;  
Best Local Similarity 27.9%; Pred. No. 9.6e-08;  
Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;

OY 2 VNLAFLIVSYITMFCISIKTALQTEVRNCGREYAVANRFFIVSDAICMIPYFV 61  
Db 446 LNVAFFLICACIKIYFAVNPPELMAT-----NKDKIKKMAILIFTDFTCMAPISF 499  
OY 62 VKILSLPRVE-IPDTMTSMIVIFFLPVNSALNPILYTLTTNFK 104  
Db 500 FAISAAFKVPLITVNSKVLVLFYPINSCANPFLYALFTKTFQ 543

RESULT 5  
US-07-757-342D-7  
Sequence 7, Application US/07757342D  
Patent No. 6218509  
GENERAL INFORMATION:  
APPLICANT: IGARASHI, Masao  
MINEGISHI, Takashi  
NAKAMURA, Kazuo  
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/757,342D  
FILING DATE: 10-Sep-1991  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BUCKLEY, Linda M.  
REGISTRATION NUMBER: 31003  
REFERENCE/DOCKET NUMBER: 41226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 636 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-07-757-342D-7

Query Match 25.2%; Score 138.5; DB 4; Length 636;  
Best Local Similarity 27.9%; Pred. No. 1e-07;  
Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;

OY 2 VNLAFLIVSYITMFCISIKTALQTEVRNCGREYAVANRFFIVSDAICMIPYFV 61  
Db 471 LNVAFFLICACIKIYFAVNPPELMAT-----NKDKIKKMAILIFTDFTCMAPISF 524  
OY 62 VKILSLPRVE-IPDTMTSMIVIFFLPVNSALNPILYTLTTNFK 104  
Db 525 FAISAAFKVPLITVNSKVLVLFYPINSCANPFLYALFTKTFQ 568

RESULT 6  
US-07-757-342D-10  
Sequence 10, Application US/07757342D  
Patent No. 6218509  
GENERAL INFORMATION:  
APPLICANT: IGARASHI, Masao  
MINEGISHI, Takashi  
NAKAMURA, Kazuo  
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/757,342D  
FILING DATE: 10-Sep-1991  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BUCKLEY, Linda M.  
REGISTRATION NUMBER: 31003  
REFERENCE/DOCKET NUMBER: 41226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 674 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-07-757-342D-10

Query Match 25.2%; Score 138.5; DB 4; Length 674;  
Best Local Similarity 27.9%; Pred. No. 1.1e-07;  
Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;

OY 2 VNLAFLIVSYITMFCISIKTALQTEVRNCGREYAVANRFFIVSDAICMIPYFV 61  
Db 509 LNVAFFLICACIKIYFAVNPPELMAT-----NKDKIKKMAILIFTDFTCMAPISF 562  
OY 62 VKILSLPRVE-IPDTMTSMIVIFFLPVNSALNPILYTLTTNFK 104  
Db 563 FAISAAFKVPLITVNSKVLVLFYPINSCANPFLYALFTKTFQ 606

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US-07-757-342D-2
; Sequence 2, Application US/07757342D
; Patent No. 6218509
GENERAL INFORMATION:
APPLICANT : IGARASHI, Masao
             MINEGISHI, Takashi
             NAKAMURA, Kazuo
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07//57,342D
FILING DATE: 10-SEP-1991
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-07-757-342D-2
Query Match      25.2%; Score 138.5; DB 4; Length 699;
Best Local Similarity 27.9%; Pred.No.1.le-07;
Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2
OY 2 VNLAFLIVESYTFMCISQKTALQTTEVRNCFGREAVANRFFFIYSDAICWIPV 61
   ::::| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 534 LNVVAFFLICACYIKIFYAVRNDELMT-----NKDTKIAKKMAILPTDCMAPISF 587
   ::::| | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 62 VKILSLRVE-LPDMTSMIVIFFLPVNSALMLPIYLTLTNFRK 104
   -:-:-| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 568 FAISAFAFPVLITVNSKVLLVLFVPINSCANPFYAIFTKTFQ 631

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STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757, 342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-07-757-342D-3

Query Match          24.9% Score 136.5; DB 4: Length 700;
Best Local Similarity 27.9%; Pred. No. 1,9e-07;
Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;

QY      2 VNLAFLIVSVITMFCSIQTALOTTEVRNCFGEVAVANRFFEVSDAICWIPVY 61
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Db      538 INVVAFFVACIYRIYFAVNDELTA-----NKDTKIAKKMAILFTDFCMAPISF 591
       |::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|

QY      62 VKILSFVE-IPTDMTSIVIFFLPVNSALNPILYTLTNNEX 104
       |::|::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db      592 PAISAFFVPLTYTNSKLTLVFYNSCANPFLAITKAQ 635

RESULT 9
US-07-741-453A-55
Sequence 55, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741, 453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER:. 16773
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REFERENCE/DOCKET NUMBER: 91913/1107/US/ST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 795 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-741-453A-55

Query Match 23.6%; Score 129.5; DB 4; Length 795;  
Best Local Similarity 27.0%; Pred. No. 1.3e-06;  
Matches 30; Conservative 25; Mismatches 43; Indels 13; Gaps 3;

QY 1 GVNLAFLIVSYITMFCSTOKTALQTEVRNCGREVAVANRFFEFVSDAICMI--- 57  
Db 614 GLNVAFVVICACYIRIYFAVNPELMAP-----NKDTKIAKKMALLIFDTFCMARI 667  
QY 58 ---FVFWKILSRVE-IPDTMTSWIYIFLPVNSALNPILYTLTTFNFK 104  
Db 668 HCGIPSEFSAARFVPLITVNSKILVLFYVNSCANPFLYAIFTKTFQ 718

RESULT 10  
US-08-118-270-53

Sequence 53, Application US/08118270  
Patent No. 5508384

GENERAL INFORMATION:

APPLICANT: Murphy, Randall B.

INVENTOR: Schuster, David I.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

NUMBER OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

CORRESPONDENCE ADDRESS: 348

ADDRESSEE: BROWDY AND NEWMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY-2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 332 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-118-270-53

Query Match 23.2%; Score 127.5; DB 1; Length 332;

Best Local Similarity 28.2%; Pred. No. 8.3e-07;  
Matches 29; Conservative 27; Mismatches 38; Indels 9; Gaps 3;

QY 2 VNLAFLIVSYITMFCSTOKTALQTEVRNCGREVAVANRFFEFVSDAICMIPV 61  
Db 173 LNVAFLICACYIRIYFAVNPEIMATNK-----DTKIALA-----ILFTDFTC-MPISF 223

QY 62 VKILSRVEIPDTMTSWIYIFLPVNSALNPILYTLTTFNFK 104  
Db 224 FAISAARFVPLITVNSKVLVLFYVNSCANPFLYAIFTKTFQ 266

RESULT 11  
PCT-US93-08528-53

Sequence 53, Application PC/TUS9308528

GENERAL INFORMATION:

APPLICANT: New York University

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

NUMBER OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

CORRESPONDENCE ADDRESS: 348

ADDRESSEE: BROWDY AND NEWMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY-2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 332 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US93-08528-53

Query Match 23.2%; Score 127.5; DB 5; Length 332;  
Best Local Similarity 28.2%; Pred. No. 8.3e-07;  
Matches 29; Conservative 27; Mismatches 38; Indels 9; Gaps 3;

QY 2 VNLAFLIVSYITMFCSTOKTALQTEVRNCGREVAVANRFFEFVSDAICMIPV 61  
Db 173 LNVAFLICACYIRIYFAVNPEIMATNK-----DTKIALA-----ILFTDFTC-MPISF 223

QY 62 VKILSRVEIPDTMTSWIYIFLPVNSALNPILYTLTTFNFK 104  
Db 224 FAISAARFVPLITVNSKVLVLFYVNSCANPFLYAIFTKTFQ 266

RESULT 12

US-08-795-876-33

Sequence 33, Application US/08795876

Patent No. 6403305

GENERAL INFORMATION:





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GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2003, 12:45:05 ; Search time 21 Seconds  
(Without alignments)  
505.308 Million cell updates/sec

Title: US-09-930-312-2

Perfect score: 549  
Sequence: 1 GVNLLAFLLIVFSYITMFCST.....NSALNPILYLTITTFKDKL 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	100.0	107	US-09-930-312-2	Sequence 2, Appl1
2	549	100.0	66	US-09-928-175-13	Sequence 13, Appl1
3	549	100.0	682	US-09-928-175-12	Sequence 12, Appl1
4	549	100.0	684	US-09-928-175-8	Sequence 8, Appl1
5	549	100.0	713	US-09-965-536A-6	Sequence 6, Appl1
6	549	100.0	718	US-09-928-175-3	Sequence 3, Appl1
7	549	100.0	730	US-09-928-175-7	Sequence 7, Appl1
8	549	100.0	737	US-09-965-536A-2	Sequence 2, Appl1
9	549	100.0	754	US-10-229-735-1	Sequence 1, Appl1
10	549	100.0	754	US-10-222-668-2	Sequence 2, Appl1
11	549	100.0	754	US-09-928-175-2	Sequence 2, Appl1
12	478	87.1	718	US-09-928-175-21	Sequence 21, Appl1
13	478	87.1	737	US-10-229-735-3	Sequence 3, Appl1
14	478	87.1	737	US-09-928-175-20	Sequence 20, Appl1
15	376	68.5	176	US-09-989-442-105	Sequence 105, Appl1
16	376	68.5	176	US-10-073-865-84	Sequence 84, Appl1
17	376	68.5	176	US-10-103-313-373	Sequence 373, Appl1
18	376	68.5	176	US-09-764-853-557	Sequence 557, Appl1
19	376	68.5	176	US-09-764-877-2009	Sequence 2009, Appl1

20	376	68.5	396	10	US-09-895-686-4	Sequence 4, Appl1
21	376	68.5	357	10	US-09-928-175-24	Sequence 24, Appl1
22	371	67.6	327	9	US-09-782-974C-66	Sequence 66, Appl1
23	234	42.6	334	9	US-10-270-333-21	Sequence 21, Appl1
24	234	42.6	722	9	US-10-222-668-4	Sequence 4, Appl1
25	225	41.0	359	9	US-10-270-333-27	Sequence 27, Appl1
26	210	38.3	1115	9	US-09-965-536A-10	Sequence 10, Appl1
27	210	38.3	1115	9	US-10-222-668-3	Sequence 3, Appl1
28	142	25.9	861	10	US-09-804-551B-20	Sequence 20, Appl1
29	138.5	25.2	456	10	US-09-862-767A-5	Sequence 5, Appl1
30	138.5	25.2	699	10	US-09-804-626-6	Sequence 6, Appl1
31	136.5	24.9	674	10	US-09-877-804-3	Sequence 3, Appl1
32	136.5	24.9	700	10	US-09-877-804-2	Sequence 2, Appl1
33	132.5	24.1	693	9	US-09-965-536A-15	Sequence 15, Appl1
34	129.5	23.6	676	9	US-09-965-536A-14	Sequence 14, Appl1
35	125	22.8	458	10	US-09-862-767A-9	Sequence 9, Appl1
36	125	22.8	695	10	US-09-804-626-8	Sequence 8, Appl1
37	124	22.6	25	9	US-09-965-536A-21	Sequence 21, Appl1
38	123	22.4	326	9	US-09-800-274-4	Sequence 4, Appl1
39	123	22.4	915	9	US-10-270-336-5	Sequence 5, Appl1
40	122	22.2	675	10	US-09-877-804-7	Sequence 7, Appl1
41	122	22.2	687	9	US-09-965-536A-13	Sequence 13, Appl1
42	122	22.2	688	9	US-09-965-536A-12	Sequence 12, Appl1
43	122	22.2	692	9	US-09-965-536A-11	Sequence 11, Appl1
44	122	22.2	692	10	US-09-877-804-6	Sequence 6, Appl1
45	120	21.9	794	9	US-10-270-336-7	Sequence 7, Appl1

## ALIGNMENTS

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RESULT 1
US-09-930-312-2
; Sequence 2, Application US/09930312
; Publication No. US20030032019A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: No. US20030032019A1 G Protein-Coupled Receptors
; FILE REFERENCE: 00329.PC1
; CURRENT APPLICATION NUMBER: US/09/930, 312
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: USSN 60/225, 262
; PRIORITY FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-312-2

Query Match      100.0%; Score 549; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 3, 9e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GVNLLAFLLIVFSYITMFCSTOKTALQTEVRNCGEVAANRFFIVSDAICWIPVF 60
Db      1 GVNLLAFLLIVFSYITMFCSTOKTALQTEVRNCGEVAANRFFIVSDAICWIPVF 60
QY      61 VKLLSFVEIPPTMTSMIYIFFLPVNSALNPILYLTITTFKDKL 107
Db      61 VKLLSFVEIPPTMTSMIYIFFLPVNSALNPILYLTITTFKDKL 107

RESULT 2
US-09-928-175-13
; Sequence 13, Application US/09928175
; Patent No. US20020123618A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
```

```
; APPLICANT: Rogers, No. US20020123618Alma
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 13
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-175-13

Query Match          100.0%; Score 549; DB 10; Length 646;
Best Local Similarity 100.0%; Pred. No. 2.7e-55;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 488 GVNLAFLIIVSYITMFCISOKTALQTEVRNCFGREVAVANRFFFIYSDAICWIPVF 547
   |||||||
QY 61 VKILSLFRVEIPDWTMTSWIVIFFLPVNSALNDILYTLTTFNFKDKL 107
   |||||||
Db 548 VKILSLFRVEIPDWTMTSWIVIFFLPVNSALNDILYTLTTFNFKDKL 594
   |||||||
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RESULT 3  
US-09-928-175-12

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; Sequence 12, Application US/09928175
; Patent No. US20020123618A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618Alma
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-175-12
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Query Match 100.0%; Score 549; DB 10; Length 682;  
Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GVNLAFLIIVSYITMFCISOKTALQTEVRNCFGREVAVANRFFFIYSDAICWIPVF 60
   |||||||
Db 524 GVNLAFLIIVSYITMFCISOKTALQTEVRNCFGREVAVANRFFFIYSDAICWIPVF 583
   |||||||
QY 61 VKILSLFRVEIPDWTMTSWIVIFFLPVNSALNDILYTLTTFNFKDKL 107
   |||||||
Db 584 VKILSLFRVEIPDWTMTSWIVIFFLPVNSALNDILYTLTTFNFKDKL 630
   |||||||
```

RESULT 4  
US-09-928-175-8  
; Sequence 8, Application US/09928175  
; Patent No. US20020123618A1  
; GENERAL INFORMATION:  
; APPLICANT: Paszty, Christopher J.  
; APPLICANT: Gong, Jianhua

```
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618Alma
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 8
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-175-8

Query Match          100.0%; Score 549; DB 10; Length 694;
Best Local Similarity 100.0%; Pred. No. 2.9e-55;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GVNLAFLIIVSYITMFCISOKTALQTEVRNCFGREVAVANRFFFIYSDAICWIPVF 60
   |||||||
Db 536 GVNLAFLIIVSYITMFCISOKTALQTEVRNCFGREVAVANRFFFIYSDAICWIPVF 595
   |||||||
QY 61 VKILSLFRVEIPDWTMTSWIVIFFLPVNSALNDILYTLTTFNFKDKL 107
   |||||||
Db 596 VKILSLFRVEIPDWTMTSWIVIFFLPVNSALNDILYTLTTFNFKDKL 642
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RESULT 5  
US-09-965-536A-6

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; Sequence 6, Application US/09965536A
; Publication No. US20030027323A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGRPMY5,
; FILE REFERENCE: D0041NP
; CURRENT APPLICATION NUMBER: US/09/965,536A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-536A-6
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Query Match 100.0%; Score 549; DB 9; Length 713;  
Best Local Similarity 100.0%; Pred. No. 3e-55;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GVNLAFLIIVSYITMFCISOKTALQTEVRNCFGREVAVANRFFFIYSDAICWIPVF 60
   |||||||
Db 555 GVNLAFLIIVSYITMFCISOKTALQTEVRNCFGREVAVANRFFFIYSDAICWIPVF 614
   |||||||
QY 61 VKILSLFRVEIPDWTMTSWIVIFFLPVNSALNDILYTLTTFNFKDKL 107
   |||||||
Db 615 VKILSLFRVEIPDWTMTSWIVIFFLPVNSALNDILYTLTTFNFKDKL 661
   |||||||
```

```

RESULT 6
US-09-928-175-3
; Sequence 3, Application US/09928175
; Patent No. US20020123618A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher J.
; APPLICANT: Gong, Jiahua
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618A1ma
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 718
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-175-3

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	Query Match	100.0%	Score 549	DB 10	Length 718
	Best Local Similarity	100.0%	Pred. No. 3e-55		
	Matches 107	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	GYNLAFLLIVSYITMRCISIOKTA	LOTTEVYRNCGR	EYAVANRFFIYFSDAIC	IPVF 60
DB	560	GYNLAFLLIVSYITMRCISIOKTA	LOTTEVYRNCGR	EYAVANRFFIYFSDAIC	IPVF 619
QY	61	VKILSFREVEIPDMTSWIV	FFLPVNSALNP	IYTLTTFEKKDL	107
DB	620	VKILSFREVEIPDMTSWIV	FFLPVNSALNP	IYTLTTFEKKDL	666

RESULT 7  
 US-09-928-175-7  
 Sequence 7, Application US/09928175  
 Patent No. US20020123618A1  
 GENERAL INFORMATION:  
 APPLICANT: Paszly, Christopher J.  
 APPLICANT: Gong, Jianhua  
 APPLICANT: Daugherty, Betsy  
 APPLICANT: Rogers, No. US20020123618A1ma  
 TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and  
 TITLE OF INVENTION: Uses Thereof  
 FILE REFERENCE: 00-1229  
 CURRENT APPLICATION NUMBER: US/09/928,175  
 CURRENT FILING DATE: 2001-08-10  
 PRIOR APPLICATION NUMBER: 60/724,455  
 PRIOR FILING DATE: 2000-08-10  
 NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 7  
 LENGTH: 730  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-928-175-7

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Query Match Similarity      100.0% Score 549 DB 10 Length 730;
Best local similarity      100.0%; Pred. No. 3 le-55;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0

          1 GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCRGREVAANRRFFIYFSDAICMIPVF 60
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 61
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 62
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 63
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 64
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 65
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 66
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 67
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 68
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 69
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 70
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 71
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 72
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 73
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 74
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 75
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 76
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 77
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 78
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 79
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 80
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 81
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 82
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 83
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 84
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 85
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 86
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 87
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 88
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 89
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 90
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 91
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 92
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 93
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 94
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 95
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 96
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 97
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 98
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 99
            GYNLAFLIYVSYYTMRFCISIOKTALQTTVEVNCGRREVAANRRFFIYFSDAICMIPVF 100

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RESULT 8
; US-09-965-536A-2
; Sequence 2, Application US/09965536A
; Publication No. US20030027323A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBRY5,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
; FILE REFERENCE: D0041NP
; CURRENT APPLICATION NUMBER: US/09/965,536A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-536A-2

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Query Match	100.0%	Score	549.	DB	9.	Length	737.
Best Local Similarity	100.0%	Pred.	No. 3.1e-55.				
Matches	107.	Conservative	0.	Mismatches	0.	Indels	0.
				Gaps			
QY	1	GYNLLAFLLIVSYITMCSIOKTLQTTVEYRNCGRVAVANRRFFVSDAICMIPVF	60				
Db	579	GYNLLAFLLIVSYITMCSIOKTLQTTVEYRNCGRVAVANRRFFVSDAICMIPVF	638				
QY	61	VVKILSLFRVEIPDPTMTSMIIVFELPVNSALNPILYTLTTTFPFDKL	107				
Db	639	VVKILSLFRVEIPDPTMTSMIIVFELPVNSALNPILYTLTTTFPFDKL	685				

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RESULT 9
US-10-229-735-1
; Sequence 1, Application US/10229735
; Publication No. US20030082650A1
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; APPLICANT: Agoulunik, Alexander I.
; TITLE OF INVENTION: The GREAT Gene and Protein
; FILE REFERENCE: 7572/73263
; CURRENT APPLICATION NUMBER: US/10/229,735
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/315,696
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/351,432
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 754
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-229-735-1

```

Query Match	100.0%;	Score 549;	DB 9;	Length 754;
Best Local Similarity	100.0%;	Pred. No. 3.2e-55;		
Matches 107;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps

QY 572 VVKILSL  
DB 61 VVKILSL  
QY 632 VVKILSL  
DB

IQKTALQTEVRNCGREAVANRFFFIYSDAICWIPVF 655  
VIFFLPVNSALNPILYTLTTFNFKDKL 107  
VIFFLPVNSALNPILYTLTTFNFKDKL 702

10222668  
184A1

APPLICANT: HSU, Shueh  
APPLICANT: Hsueh, Aaron  
TITLE OF INVENTION: Mammalian Relaxin Receptor  
FILE REFERENCE: STAN-239 WO  
CURRENT APPLICATION NUMBER: US/10/222,668  
CURRENT FILING DATE: 2002-08-15  
PRIOR APPLICATION NUMBER: 60/313,259  
PRIOR FILING DATE: 2002-08-17  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version.4.0  
SEQ ID NO 2  
LENGTH: 754  
TYPE: PRT  
ORGANISM: H. sapiens  
US-10-222-668-2

Query Match 100.0%; Score 549; DB 9; Length 754;  
Best Local Similarity 100.0%; Pred. No. 3.2e-55;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVNLAFLIIVFSYITMFCISOKTALQTEVRNCGREAVANRFFFIYSDAICWIPVF 60  
DB 596 GVNLAFLIIVFSYITMFCISOKTALQTEVRNCGREAVANRFFFIYSDAICWIPVF 655  
QY 61 VVKILSLFVEIPDPTMTSWIVFFLPVNSALNPILYTLTTFNFKDKL 107  
DB 656 VVKILSLFVEIPDPTMTSWIVFFLPVNSALNPILYTLTTFNFKDKL 702

RESULT 11  
US-09-928-175-2  
Sequence 2, Application US/09928175  
Patent No. US20020123618A1  
GENERAL INFORMATION:  
APPLICANT: Paszty, Christopher J.  
APPLICANT: Gong, Jianhua  
APPLICANT: Daugherty, Betsy  
TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and  
FILE REFERENCE: 00-1229  
CURRENT APPLICATION NUMBER: US/09/928,175  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/224,455  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 754  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-928-175-2

Query Match 100.0%; Score 549; DB 10; Length 754;  
Best Local Similarity 100.0%; Pred. No. 3.2e-55;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 VVKILSLFVEIPDPTMTSWIVFFLPVNSALNPILYTLTTFNFKDKL 107  
DB 656 VVKILSLFVEIPDPTMTSWIVFFLPVNSALNPILYTLTTFNFKDKL 702

RESULT 12  
US-09-928-175-21  
Sequence 21, Application US/09928175  
Patent No. US20020123618A1  
GENERAL INFORMATION:  
APPLICANT: Paszty, Christopher J.  
APPLICANT: Gong, Jianhua  
APPLICANT: Daugherty, Betsy  
TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and  
FILE REFERENCE: 00-1229  
CURRENT APPLICATION NUMBER: US/09/928,175  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/224,455  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 21  
LENGTH: 718  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-928-175-21

Query Match 87.1%; Score 478; DB 10; Length 718;  
Best Local Similarity 86.0%; Pred. No. 4.7e-47;  
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 GVNLAFLIIVFSYITMFCISOKTALQTEVRNCGREAVANRFFFIYSDAICWIPVF 60  
DB 560 GVNLAFLIIVFSYITMFCISOKTALQTEVRNCGREAVANRFFFIYSDAICWIPVF 619  
QY 61 VVKILSLFVEIPDPTMTSWIVFFLPVNSALNPILYTLTTFNFKDKL 107  
DB 620 VVKILSLFVEIPDPTMTSWIVFFLPVNSALNPILYTLTTFNFKDKL 666

RESULT 13  
US-10-229-735-3  
Sequence 3, Application US/10229735  
Publication No. US20030082650A1  
GENERAL INFORMATION:  
APPLICANT: Baylor College of Medicine  
APPLICANT: Agoulnik, Alexander I.  
TITLE OF INVENTION: The GREAT Gene and Protein  
FILE REFERENCE: 7572/73263  
CURRENT APPLICATION NUMBER: US/10/229,735  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 60/315,696  
PRIOR FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: 60/351,432  
PRIOR FILING DATE: 2002-01-28  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 737  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-229-735-3

Query Match 87.1%; Score 478; DB 9; Length 737;  
Best Local Similarity 86.0%; Pred. No. 4.9e-47;  
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 GVNLAFLIIVFSYITMFCISOKTALQTEVRNCGREAVANRFFFIYSDAICWIPVF 60  
DB 579 GVNLAFLIIVFSYITMFCISOKTALQTEVRNCGREAVANRFFFIYSDAICWIPVF 638



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QY 61 VKILSLFVEIPDTMTSMIVIFFLPVNSALNPILYTLTTFEFDKL 107
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 639 VKILSLQVEIPGTITSMIVFELPVNSALNPILYTLTTSFFFDKL 685

RESULT 14
US-09-928-175-20
; Sequence 20, Application US/09928175
; Patent No. US20020123618A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618Alma
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-928-175-20

Query Match 87.1%; Score 478; DB 10; Length 737;
Best Local Similarity 86.0%; Pred. No. 4.9e-47;
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 GVNLAFLIVFSYITMFCSTOKTALOTTEVRNCGREVAVANFEFFIVSDAICWIPVF 60
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 579 GVNLAFLVIVISYITMFCSTHKTALOTAEVRSHIGREVAVANFEFFIVSDAICWIPVF 638

QY 61 VVILSLFVEIPDTMTSMIVIFFLPVNSALNPILYTLTTFEFDKL 107
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 639 VVILSLQVEIPGTITSMIVFELPVNSALNPILYTLTTSFFFDKL 685

RESULT 15
US-09-989-442-105
; Sequence 105, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ208
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
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; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
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PRIOR APPLICATION NUMBER: 60/237, 040	PRIOR FILING DATE: 2000-10-02	PRIOR APPLICATION NUMBER: 60/240, 960	PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: 60/239, 935	PRIOR FILING DATE: 2000-10-13	PRIOR APPLICATION NUMBER: 60/223, 937	PRIOR FILING DATE: 2000-10-13	PRIOR APPLICATION NUMBER: 60/244, 787	PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: 60/246, 474	PRIOR FILING DATE: 2000-11-08	PRIOR APPLICATION NUMBER: 60/246, 532	PRIOR FILING DATE: 2000-11-08	PRIOR APPLICATION NUMBER: 60/249, 216	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 210	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/226, 681	PRIOR FILING DATE: 2000-08-22	PRIOR APPLICATION NUMBER: 60/225, 759	PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/225, 213	PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/227, 182	PRIOR FILING DATE: 2000-08-22	PRIOR APPLICATION NUMBER: 60/225, 214	PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/235, 836	PRIOR FILING DATE: 2000-09-27	PRIOR APPLICATION NUMBER: 60/230, 438	PRIOR FILING DATE: 2000-09-06	PRIOR APPLICATION NUMBER: 60/215, 135	PRIOR FILING DATE: 2000-06-30	PRIOR APPLICATION NUMBER: 60/225, 266	PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/249, 218	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 208	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 213	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 212	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 207	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 245	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 244	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 217	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 211	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 215	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 284	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 242	PRIOR FILING DATE: 2000-09-14	PRIOR APPLICATION NUMBER: 60/231, 242	PRIOR FILING DATE: 2000-09-08	PRIOR APPLICATION NUMBER: 60/232, 081	PRIOR FILING DATE: 2000-09-08	PRIOR APPLICATION NUMBER: 60/233, 080	PRIOR FILING DATE: 2000-09-08	PRIOR APPLICATION NUMBER: 60/231, 414	PRIOR APPLICATION NUMBER: 60/231, 244
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1 PRIOR FILING DATE: 2000-09-08  
2 PRIOR APPLICATION NUMBER: 60/233,066  
3 PRIOR FILING DATE: 2000-09-14  
4 PRIOR APPLICATION NUMBER: 60/233,063  
5 PRIOR FILING DATE: 2000-09-14  
6 PRIOR APPLICATION NUMBER: 60/232,397  
7 PRIOR FILING DATE: 2000-09-14  
8 PRIOR APPLICATION NUMBER: 60/232,399  
9 PRIOR FILING DATE: 2000-09-14  
10 PRIOR APPLICATION NUMBER: 60/232,401  
11 PRIOR FILING DATE: 2000-09-14  
12 PRIOR APPLICATION NUMBER: 60/232,400  
13 PRIOR FILING DATE: 2000-09-14  
14 PRIOR APPLICATION NUMBER: 60/241,808  
15 PRIOR FILING DATE: 2000-10-20  
16 PRIOR APPLICATION NUMBER: 60/241,828  
17 PRIOR FILING DATE: 2000-10-20  
18 PRIOR APPLICATION NUMBER: 60/241,786  
19 PRIOR FILING DATE: 2000-10-20  
20 PRIOR APPLICATION NUMBER: 60/241,788  
21 PRIOR FILING DATE: 2000-10-20  
22 PRIOR APPLICATION NUMBER: 60/241,221  
23 PRIOR FILING DATE: 2000-10-20  
24 PRIOR APPLICATION NUMBER: 60/246,475  
25 PRIOR FILING DATE: 2000-11-08  
26 PRIOR APPLICATION NUMBER: 60/231,244  
27 PRIOR FILING DATE: 2000-09-08  
28 PRIOR APPLICATION NUMBER: 60/233,065  
29 PRIOR FILING DATE: 2000-09-14

Query Match	68.5%;	Score 376;	DB 9;	Length 176;
Best Local Similarity	64.5%;	Pred. No. 6.1e-36;		
Matches	69;	Conservative	20;	Mismatches 18;
			Indels	0;
			Gaps	0

[illegible]

Search completed: May 22, 2003, 12:48:58  
Job time : .22 secs

PRIOR APPLICATION NUMBER: 60/237, 040	PRIOR FILING DATE: 2000-10-02	PRIOR APPLICATION NUMBER: 60/240, 960	PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: 60/239, 935	PRIOR FILING DATE: 2000-10-13	PRIOR APPLICATION NUMBER: 60/223, 937	PRIOR FILING DATE: 2000-10-13	PRIOR APPLICATION NUMBER: 60/244, 787	PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: 60/246, 474	PRIOR FILING DATE: 2000-11-08	PRIOR APPLICATION NUMBER: 60/246, 532	PRIOR FILING DATE: 2000-11-08	PRIOR APPLICATION NUMBER: 60/249, 216	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 210	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/226, 681	PRIOR FILING DATE: 2000-08-22	PRIOR APPLICATION NUMBER: 60/225, 759	PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/225, 213	PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/227, 182	PRIOR FILING DATE: 2000-08-22	PRIOR APPLICATION NUMBER: 60/225, 214	PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/235, 836	PRIOR FILING DATE: 2000-09-27	PRIOR APPLICATION NUMBER: 60/230, 438	PRIOR FILING DATE: 2000-09-06	PRIOR APPLICATION NUMBER: 60/215, 135	PRIOR FILING DATE: 2000-06-30	PRIOR APPLICATION NUMBER: 60/225, 266	PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/249, 218	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 208	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 213	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 212	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 207	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 245	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 244	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 217	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 211	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 215	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 284	PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249, 242	PRIOR FILING DATE: 2000-09-14	PRIOR APPLICATION NUMBER: 60/231, 242	PRIOR FILING DATE: 2000-09-08	PRIOR APPLICATION NUMBER: 60/232, 081	PRIOR FILING DATE: 2000-09-08	PRIOR APPLICATION NUMBER: 60/233, 080	PRIOR FILING DATE: 2000-09-08	PRIOR APPLICATION NUMBER: 60/231, 414	PRIOR APPLICATION NUMBER: 60/231, 244
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GenCore version 5.1.4-p5.4578  
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## OM protein - protein search, using sw model

Run on: May 22, 2003, 12:43:05 ; Search time 43 Seconds  
(without alignments)  
239.218 Million cell updates/sec

Title: US-09-930-312-2

Perfect score: 549

Sequence: 1 GVNLAFLIVFSYITMFCSS.....NSALNPILYTLTTFNKDKL 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	210	38.3	1115	2 S40241	G protein-coupled
2	145.5	26.5	320	2 S17177	probable G protein
3	145.5	26.5	337	2 S68678	adenosine receptor
4	139.5	25.4	966	2 A41344	lutropin-choriogon
5	139	25.2	925	2 JC2033	G protein-coupled
6	138.5	25.2	320	2 A46152	A3 adenosine recep
7	138.5	25.2	699	1 ORHUT	lutropin-choriogon
8	136.5	24.9	700	2 I77463	lutelinizing hormon
9	136.5	24.9	700	2 A49744	lutropin-choriogon
10	135.5	24.7	814	2 JC7389	thyroid stimulatn
11	134.5	24.5	793	2 A42390	thyroid stimulatn
12	132.5	24.1	700	2 A4395	lutropin receptor
13	132	24.0	694	2 JC4301	folliotropin recept
14	129	23.5	694	2 JC2237	folliotropin recept
15	125.5	22.9	696	2 JC7361	folliotropin recept
16	125	22.8	695	1 ORHUT	folliotropin recept
17	125	22.8	695	1 I45896	follicle stimulat
18	125	22.8	695	2 JC1493	folliotropin recept
19	124	22.6	326	2 I48096	A1 adenosine recep
20	123	22.4	326	2 A53005	adenosine receptor
21	122	22.2	692	2 A34548	folliotropin recept
22	122	22.2	695	1 JN0898	folliotropin recept
23	121	22.0	324	2 S55302	A(1) adenosine rec
24	120.5	21.9	764	2 A40077	thyrotropin recept
25	120.5	21.9	764	2 JC5643	thyroid stimulatn
26	120	21.9	185	2 I48931	adenosine receptor
27	120	21.9	326	2 A40376	adenosine receptor
28	119.5	21.8	318	2 S38511	adenosine receptor
29	119.5	21.8	764	1 ORHUT	thyrotropin recept

30	119.5	21.8	764	2 A35956	thyrotropin recept
31	119	21.7	326	2 C30341	G protein-coupled
32	119	21.7	332	2 I48933	adenosine receptor
33	119	21.7	907	2 JG0193	G protein-coupled
34	118.5	21.6	764	2 I48882	thyrotropin recept
35	117	21.3	326	2 A38144	adenosine receptor
36	116	21.1	332	2 A42171	A2-adenosine recep
37	115	20.9	372	2 JC1229	adenosine receptor
38	114	20.8	328	2 JN0675	adenosine receptor
39	110	20.0	907	2 JE0176	orphan G protein-c
40	109.5	19.9	328	2 T30999	hypothetical prote
41	108	19.7	391	2 A41795	somatostatin recep
42	108	19.7	391	2 C41795	somatostatin recep
43	108	19.7	391	2 A39297	somatostatin recep
44	107	19.5	386	2 S72168	dopamine receptor
45	105.5	19.2	381	2 A35300	G protein-coupled

## ALIGNMENTS

RESULT 1  
S40241  
G protein-coupled receptor - great pond snail  
C:Species: Lymnaea stagnalis (great pond snail)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 15-Jun-2001  
C:Accession: S40241  
R/Tensen, C.P.; Kesteren, E.R.; Planta, R.J.; Cox, K.; Burke, J.F.; Heerikhuizen, H.;  
submitted to the EMBL Data Library, June 1993  
A:Description: A G protein-coupled receptor with LDL-binding motifs suggests a role f  
A:Reference number: S40241  
A:Accession: S40241  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1115 <TEN>  
A:Cross-references: EMBL:223104; NID:9438128; PID:9438129  
C:Superfamily: great pond snail LDL receptor-related G protein-coupled receptor; LDL  
C:Keywords: G protein-coupled receptor; transmembrane protein  
F:38-77/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F:79-113/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F:118-153/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F:158-194/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F:195-230/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
F:233-267/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
F:274-316/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F:322-361/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
F:367-401/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
F:406-440/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
F:446-483/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F:488-523/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
F:584-607/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:608-631/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:632-655/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:656-679/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:704-727/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:774-797/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

Query Match 38.3%; Score 210; DB 2; Length 1115;  
Best Local Similarity 41.6%; Pred. No. 4, 2e-15;  
Matches 42; Conservative 23; Mismatches 30; Indels 6; Gaps 2;

QY 2 VNLAFILIVFSYITMFCSSIOKT--ALQTEVNRNCFREYAVANRFFIYFSPAICIPV 59  
DB 946 LNLSEVLINSLTLMFESVAKKTRSAVTRAESKN----DNAMARKMLIYITDPCWVPI 1001

QY 60 FVVKILSLFRLVETPDWTMTSNVIFFLPVNSALNPILYTLTT 100  
DB 1002 IIVGFVSLAGARADQGVYVIAVFLPLNSATNPVITYLTST 1042

RESULT 2  
S17177  
probable G protein-coupled receptor - rat



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RESULT 6
A46152
A3:adenosine receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999
C:Accession: A46152
R:Zhou, Q.Y.; Li, C.; Olah, M.E.; Johnson, R.A.; Stiles, G.L.; Civelli, O.
Proc. Natl. Acad. Sci. U.S.A. 89, 7432-7436, 1992
A:Title: Molecular cloning and characterization of an adenosine receptor: the A3 adenosine
A:Reference number: A46152; MIMD:92366475; PMID:1323836
A:Accession: A46152
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-320 <ZHO>
A:Cross-references: GB:M94152; NID:g202724; PIDN:AAA0680.1; PID:g460332
A:Experimental source: brain
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:110661, NCBIP:110662)
C:Superfamily: adenosine receptor A1
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      25.2%; Score 138.5; DB 2; Length 320;
Best Local Similarity 29.9%; Pred. No. 9.4e-08;
Matches 29; Conservative 22; Mismatches 41; Indels 5; Gaps 2;

QY 4 LLAFLIVEGYITMFCSTOKTALQT---TEVRNCFGEVAVANRFFVFSDAICWIPV 59
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 189 LIPLVVMCIITLDFTYIRKLSQNLGFRFTRAFYGRFKTAKSLFLVFLPALCMLPL 248
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 60 FVVKILSFRVEIPDPTMTSWIYFFLPVNSALNPILY 96
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 249 SINFVSYFNVKIPKE-IAMCGILLSHANSMMNPILY 284
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 7
QRHNU
Lutropin-choriogonadotropin receptor precursor - human
N:Alternate names: luteinizing hormone-choriogonadotropin receptor
N:Contents: lutropin-choriogonadotropin receptor precursor long splice form; lutropin-ch
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 16-Feb-1996 #text_change 22-Jun-1999
C:Accession: A36243; B36243; A23728; B36120
R:Minagishi, T.; Nakamura, K.; Takakura, Y.; Miyamoto, K.; Hasegawa, Y.; Ibuki, Y.; Igara
Biochem. Biophys. Res. Commun. 172, 1049-1054, 1990
A:Title: Cloning and sequencing of human LH/hCG receptor cDNA.
A:Reference number: A36243; MIMD:91058534; PMID:2244680
A:Accession: A36243
A:Molecule type: mRNA
A:Residues: 1-699 <MIN>
A:Cross-references: GB:M63108; NID:g187135; PIDN:AAA59515.1; PID:g187136
A:Experimental source: ovary
A:Accession: B36243
A:Molecule type: mRNA
A:Residues: 1-226,290-699 <MID>
R:Jia, X.C.; Oikawa, M.; Bo, M.; Tanaka, T.; Ny, T.; Bolme, I.; Hsueh, A.J.W.
Mol. Endocrinol. 5, 759-768, 1991
A:Title: Expression of human luteinizing hormone (LH) receptor: interaction with LH and
A:Reference number: A23728; MIMD:92017881; PMID:1922095
A:Accession: A23728
A:Molecule type: mRNA
A:Residues: 1-123, 'R', 125-311, 'N', 313-699 <JIA>
A:Cross-references: GB:S57793
A:Experimental source: ovary granulosa and luteal cells; thyroid
A>Note: 312-ser was also found; the authors translated the codon UAC for residue 546 as
A>Note: mRNA from the thyroid is incompletely processed compared with that from the ova
R:Frazier, A.L.; Robbins, L.S.; Stork, P.J.; Sprengel, R.; Segaloff, D.L.; Cone, R.D.
Mol. Endocrinol. 4, 1264-1276, 1990
A:Title: Isolation of TSH and LH/CG receptor cDNAs from human thyroid: regulation by t
A:Reference number: A36120; MIMD:91155962; PMID:2293030
A:Accession: B36120
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-6, 'P', 8-18, 'A', 20-26, 'R', 29-43, 'A', 45, 'A', 47, 'RPS', 52-67, 'S', 69-123, 'R', 12

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A:Cross-references: GB:M73746; NID:g903745; PIDN:AAA70231.1; PID:g903746
A:Experimental source: thyroid
R:Zhu, H.; Wang, H.; Ascoli, M.
Mol. Endocrinol. 9, 141-150, 1995
A:Title: The lutropin/choriogonadotropin receptor is palmitoylated at intracellular c
A:Reference number: A57564; MIMD:95295727; PMID:7776964
A:Contents: annotation; mutation analysis of palmitate binding sites
C:Genetics:
A:Gene: GDB:LHRCR
A:Cross-references: GDB:125260; OMIM:152790
A:Map position: 2p21-2p21
A:Introns: 226/3
A>Note: the exact position of the intron cannot be determined from the experimental d
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repea
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone r
F:1-699/Product: lutropin-choriogonadotropin receptor precursor; long splice form #st
F:1-226,290-699/Product: lutropin-choriogonadotropin receptor precursor, short splice
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-644/Product: lutropin-choriogonadotropin receptor #status predicted <MB>
F:23-363/Domain: extracellular hormone binding #status predicted <RHB>
F:50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:74-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:99-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:124-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:149-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:176-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:198-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:364-385/Domain: transmembrane #status predicted <TM1>
F:386-418/Domain: transmembrane #status predicted <TM2>
F:441-462/Domain: transmembrane #status predicted <TM3>
F:483-505/Domain: transmembrane #status predicted <TM4>
F:526-547/Domain: transmembrane #status predicted <TM5>
F:571-594/Domain: transmembrane #status predicted <TM6>
F:606-627/Domain: transmembrane #status predicted <TM7>
F:645-699/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:99,174,195,291,313/Binding site: carbohydrate (Asn) (covalent) #status predicte
F:561,677/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pred
F:643,644/Binding site: palmitate (Cys) (covalent) #status experimental
F:670/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte

Query Match      25.2%; Score 138.5; DB 1; Length 699;
Best Local Similarity 27.9%; Pred. No. 2e-07;
Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;

QY 2 VNLLAFILFYSTYTMFCSTOKTALQTEVRNCFGEVAVANRFFVFSDAICWIPV 61
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 534 LNVVAFPIICACYKIRIFAVANRPELMAT-----NKDKTKAKKMAIIFFDFTCMAPISF 587
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 62 VKILSFRVE-IPDPTMTSWIYFFLPVNSALNPILYLTTFNFK 104
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 588 FAISAAKVPILITYTNSKVLVLFYPINSCANPLVIAIFKTRFO 631
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 8
I177463
luteinizing hormone/chorionic gonadotropin receptor - rat
C:Species: Rattus sp. (rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C:Accession: I177463
R:Aatsinki, J.T.; Pietila, E.M.; Lakkakorpi, J.T.; Rajanleml, H.J.
Mol. Cell. Endocrinol. 84, 127-135, 1992
A:Title: Expression of the LH/CG receptor gene in rat ovarian tissue is regulated by
A:Reference number: I57668; MIMD:92347604; PMID:1353463
A:Accession: I177463
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-700 <RES>
A:Cross-references: GB:S40803; NID:g252163; PIDN:AAB2680.1; PID:g252164
C:Genetics:
A:Introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repea
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

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Query Match          24.9%; Score 136.5; DB 2; Length 700;
Best Local Similarity 27.9%; Pred. No. 3.4e-07;
Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;

OY 2 VNLAFLIIVFSYITMFCISQKTALQTTEVRNCGREAVANRPFIVSDAICWIPFV 61
DB 538 LNVAAEVVICACIRIYFAQNDELTP-----NKDTKAKMALLIFDFTCMAPISF 591

OY 62 VKILSFRE-IPDTMTSWIVFPLVNSALNPILYLTNTNFRK 104
DB 592 FAISAAFKVPLIVTNSKILLVLFYPVNSCANPFLVAIFKARQ 635

RESULT 9
A:9744
luteolin-choriogonadotropin receptor precursor - rat
N:Alternate names: luteinizing hormone-choriogonadotropin receptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-May-1994 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: A49744; A40545; A41343; A61453; A32460
R:Koo, Y. B.; Ji, I.; Slaughter, R. G.; Ji, T. H.
Endocrinology 128, 2297-2308, 1991
A:Title: Structure of the luteinizing hormone receptor gene and multiple exons of the co
A:Reference number: A49744; MUID:91209270; PMID:2019252
A:Accession: A49744
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-700 <KCE>
A:Cross-references: GB:M68917
A:Note: Authors translated the codon CAA for residue 307 as Glu, AAC for residue 355 as
R:Tsal-Morris, C. H.; Buczko, E.; Wang, W.; Xie, X. Z.; Dufau, M. L.
J. Biol. Chem. 266, 11355-11359, 1991
A:Title: Structural organization of the rat luteinizing hormone (LH) receptor gene.
A:Reference number: A40545; MUID:91250455; PMID:2040640
A:Accession: A40545
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <TSA>
A:Cross-references: GB:M63918; GB:M63919; GB:M63920; GB:M63921; GB:M63922; GB:M63923; GB
R:McFarland, K. C.; Sprengel, R.; Phillips, H. S.; Koehler, M.; Rosenblit, N.; Nikolics, R
Science 245, 494-499, 1989
A:Title: Luteolin-choriogonadotropin receptor: an unusual member of the G protein-couple
A:Reference number: A41343; MUID:89332512; PMID:2502842
A:Accession: A41343
A:Molecule type: mRNA
A:Residues: 1-700 <KCE>
A:Cross-references: GB:M61199; MUID:9205178; PIDN:AAA1528.1; PID:9205179
R:Dufau, M. L.; Minegishi, T.; Buczko, E. S.; Delgado, C. J.; Zhang, R.
J. Steroid Biochem. 33, 715-720, 1989
A:Title: Characterization and structure of ovarian and testicular LH/hCG receptors.
A:Reference number: A61453; MUID:90097014; PMID:2601325
A:Accession: A61453
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-33; 'X', 35-37, 'X', 39, 'X', 41-44 <DUF>
R:Roche, P. C.; Ryan, R. J.
J. Biol. Chem. 264, 4636-4641, 1989
A:Title: Purification, characterization, and amino-terminal sequence of rat ovarian recep
A:Reference number: A32460; MUID:89174723; PMID:2925659
A:Accession: A32460
A:Molecule type: protein
A:Residues: 27-32, 'LX', 35-37 <ROC>
C:Genetics:
A:introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone rec
F:54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:103-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

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F:368-389/Domain: transmembrane #status predicted <TM1>
F:400-422/Domain: transmembrane #status predicted <TM2>
F:444-466/Domain: transmembrane #status predicted <TM3>
F:489-511/Domain: transmembrane #status predicted <TM4>
F:530-551/Domain: transmembrane #status predicted <TM5>
F:575-598/Domain: transmembrane #status predicted <TM6>
F:610-631/Domain: transmembrane #status predicted <TM7>
F:103,178,199,295,303,317/Binding site: carbohydrate (Asn) (covalent) #status predict
F:647,648/Binding site: palmitate (Cys) (covalent) #status predicted
F:681/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte

Query Match          24.9%; Score 136.5; DB 2; Length 700;
Best Local Similarity 27.9%; Pred. No. 3.4e-07;
Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;

OY 2 VNLAFLIIVFSYITMFCISQKTALQTTEVRNCGREAVANRPFIVSDAICWIPFV 61
DB 538 LNVAAEVVICACIRIYFAQNDELTP-----NKDTKAKMALLIFDFTCMAPISF 591

OY 62 VKILSFRE-IPDTMTSWIVFPLVNSALNPILYLTNTNFRK 104
DB 592 FAISAAFKVPLIVTNSKILLVLFYPVNSCANPFLVAIFKARQ 635

RESULT 10
JC7389
thyroid stimulating hormone receptor a - salmon
N:Alternate names: thyrotropin receptor a
C:Species: Oncorhynchus sp. (salmon)
C>Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000
C:Accession: J07389
R:Oba, Y.; Hirai, T.; Yoshitake, Y.; Kobayashi, T.; Nagahama, Y.
Biochem. Biophys. Res. Commun. 276, 258-263, 2000
A:Title: Cloning, functional characterization, and expression of thyrotropin receptor
A:Reference number: JC7389
A:Contents: Thyroid
A:Accession: J07389
A:Molecule type: mRNA
A:Residues: 1-814 <OBA>
A:Cross-references: DDBJ:AB030954
C:Comment: This receptor, a transmembrane protein, which mediates the actions of thy
C:Genetics:
A:Gene: tsh-ra
A:introns: 610/3
C:Keywords: glycoprotein; hormone receptor; thyroid gland; transmembrane protein

Query Match          24.7%; Score 135.5; DB 2; Length 814;
Best Local Similarity 27.9%; Pred. No. 5.1e-07;
Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;

OY 2 VNLAFLIIVFSYITMFCISQKTALQTTEVRNCGREAVANRPFIVSDAICWIPV-F 60
DB 634 LNTLAEVLICACYIKIYCVHNPHYRSG-----SKDTNKKMAVLIFDFTCMAPISF 687

OY 61 VKILSFREIPDTMTSWIVFPLVNSALNPILYLTNTNFRK 104
DB 688 YAMSAYLDRPLIVSNSKILLVLFYPVNSCANPFLVAIFKARF 731

RESULT 11
JC7390
thyroid stimulating hormone receptor b - salmon
N:Alternate names: thyrotropin receptor b
C:Species: Oncorhynchus sp. (salmon)
C>Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000
C:Accession: J07390
R:Oba, Y.; Hirai, T.; Yoshitake, Y.; Kobayashi, T.; Nagahama, Y.
Biochem. Biophys. Res. Commun. 276, 258-263, 2000
A:Title: Cloning, functional characterization, and expression of thyrotropin receptor
A:Reference number: JC7389
A:Contents: Thyroid
A:Accession: J07390
A:Molecule type: mRNA

```

A:Residues: 1-793 <OBA>  
A:Cross-references: DDBJ:AB030955  
C:Comment: This receptor, a transmembrane protein, which mediates the actions of thyrotropin-releasing hormone.  
C:Genetics:  
A:Gene: tsh-rb  
A:Introns: 584/3  
C:Keywords: glycoprotein; hormone receptor; thyroid gland; transmembrane protein

Query Match 24.5%; Score 134.5; DB 2; Length 793;  
Best Local Similarity 27.6%; Pred. No. 6.4e-07;  
Matches 29; Conservative 25; Mismatches 42; Indels 9; Gaps 3;

QY 2 VNLAFLIIFYSTYTMCSIOKTAQTQTEVNRG-REVAANRFFIVSDAICWIPV-59  
DB 608 LNLAFLVIGCYKIKCAVHNPNY-----CGSKMDTNKAKMALIFDFLCMAPIS 660  
QY 60 FVVKILSLFVEIPDITMSVIVFPLVNSALNPIYLTITNFK 104  
DB 661 FYAMSAVDRPLIVNSKILVFLPNSCANPFLVAFYTKAER 705

## RESULT 12

A42395  
Luteinizing hormone-releasing hormone receptor  
N:Alternate names: luteinizing hormone-choriogonadotropin receptor  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Aug-1999  
C:Accession: A42395  
R:Gudermann, T.; Birnbaumer, M.; Birnbaumer, L.  
J. Biol. Chem. 267, 4479-4488, 1992  
A:Title: Evidence for dual coupling of the murine luteinizing hormone receptor to adenylyl cyclase.  
A:Reference number: A42395; MUID:92165799; PMID:1311310

A:Accession: A42395  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-700 <GUD>  
A:Cross-references: GB:M81310; GB:M81318; NID:9198811; PIDN:AAA39432.1; PID:9198812  
A:Note: sequence extracted from NCBI backbone (NCBI:84064, NCBI:84066)  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
C:Keywords: G protein-coupled receptor; transmembrane protein  
F:34-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:103-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

Query Match 24.1%; Score 132.5; DB 2; Length 700;  
Best Local Similarity 26.9%; Pred. No. 9.4e-07;  
Matches 28; Conservative 25; Mismatches 44; Indels 7; Gaps 2;

QY 2 VNLAFLIIFYSTYTMCSIOKTAQTQTEVNRG-REVAANRFFIVSDAICWIPV 61  
DB 538 LNLAFLVIGCYKIKCAVHNPNY-----CGSKMDTNKAKMALIFDFLCMAPIS 591  
QY 62 VKILSLFVEIPDITMSVIVFPLVNSALNPIYLTITNFK 104  
DB 592 FAISAAKVPILITVNSKILVFLPNSCANPFLVAFYTKAFO 635

## RESULT 13

JCA301  
Follicle-stimulating hormone receptor  
N:Alternate names: follicle-stimulating hormone receptor  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 21-Jan-2000  
C:Accession: JCA301  
R:Remy, J.J.; Labhiti-Mansats, Y.; Verle, M.; Bozon, V.; Couture, L.; Pajot, E.; Grebert, A.; Title: The porcine follicle-stimulating hormone receptor: cDNA cloning, functional expression and chromosomal localization.  
A:Reference number: JCA301; MUID:96011644; PMID:7590277

A:Accession: JCA301  
A:Molecule type: mRNA  
A:Residues: 1-694 <REM>  
A:Cross-references: GB:U31966  
A:Experimental source: ovarian granulosa cells  
C:Comment: This receptor belongs to the family of the G-protein coupled receptors. It is involved in the regulation of oogenesis in female.  
C:Genetics:

A:Gene: fshr  
A:Map position: 3 q2.2-q2.3  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein  
F:1-365/Domain: follicle-stimulating hormone binding #status predicted <HOB>  
F:70-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>  
F:366-388/Domain: transmembrane #status predicted <TM1>  
F:389-420/Domain: transmembrane #status predicted <TM2>  
F:443-464/Domain: transmembrane #status predicted <TM3>  
F:485-507/Domain: transmembrane #status predicted <TM4>  
F:528-549/Domain: transmembrane #status predicted <TM5>  
F:573-596/Domain: transmembrane #status predicted <TM6>  
F:608-629/Domain: transmembrane #status predicted <TM7>

Query Match 24.0%; Score 132; DB 2; Length 694;  
Best Local Similarity 26.4%; Pred. No. 1.1e-06;  
Matches 28; Conservative 29; Mismatches 41; Indels 8; Gaps 3;

QY 2 VNLAFLIIFYSTYTMCSIOKTAQTQTEVNRG-REVAANRFFIVSDAICWIPV 61  
DB 536 LNLAFLVIGCYKIKCAVHNPNY-----CGSKMDTNKAKMALIFDFLCMAPIS 589  
QY 62 VKILSLFVEIPDITMSVIVFPLVNSALNPIYLTITNFK 105  
DB 590 FAISAAKVPILITVNSKILVFLPNSCANPFLVAFYTKAFO 635

## RESULT 14

JC2237  
Follicle-stimulating hormone receptor - horse  
N:Alternate names: FSHR  
C:Species: Equus caballus (domestic horse)  
C:Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 13-Aug-1999  
C:Accession: JC2237; JC2370  
R:Robert, P.; Amselem, S.; Christol, S.; Benflia, J.L.; Ballet, D.; Koman, A.; Bid  
Biochem. Biophys. Res. Commun. 201, 201-207, 1994  
A:Title: Cloning and sequencing of the equine testicular follicle-stimulating hormone receptor.  
A:Reference number: JC2237; MUID:94256980; PMID:8198575

A:Accession: JC2237  
A:Molecule type: mRNA  
A:Residues: 1-694 <ROB>  
A:Cross-references: GB:S70150; NID:9546896; PIDN:AAB30854.1; PID:9546897  
A:Experimental source: testis  
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat  
C:Keywords: glycoprotein; hormone receptor; transmembrane protein  
F:56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:366-386/Domain: transmembrane #status predicted <TM1>  
F:389-420/Domain: transmembrane #status predicted <TM2>  
F:443-464/Domain: transmembrane #status predicted <TM3>  
F:485-507/Domain: transmembrane #status predicted <TM4>  
F:528-549/Domain: transmembrane #status predicted <TM5>  
F:573-596/Domain: transmembrane #status predicted <TM6>  
F:608-629/Domain: transmembrane #status predicted <TM7>  
F:608-629/Domain: transmembrane #status predicted <TM7>

Query Match 23.5%; Score 129; DB 2; Length 694;  
Best Local Similarity 27.4%; Pred. No. 2.3e-06;  
Matches 29; Conservative 27; Mismatches 42; Indels 8; Gaps 3;





GenCore version 5.1.4.p5.4578  
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# OM protein - protein search, using sw model

Run on: May 22, 2003, 12:34:09 ; Search time 25 Seconds  
(without alignments)  
177.519 Million cell updates/sec

Title: US-09-930-312-2

Perfect score: 549  
Sequence: 1 GVNLAFLIVSYITMPCS.....NSALNPILTITTFKDKL 107

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	549	100.0	754	1	LGR8_HUMAN
2	478	87.1	737	1	LGR8_MOUSE
3	376	68.5	757	1	LGR7_HUMAN
4	210	38.3	1115	1	GPCR_LYMT
5	146.5	26.7	319	1	AA3R_MOUSE
6	145.5	26.5	320	1	AA3R_RAT
7	145.5	26.5	701	1	LSHR_BOVIN
8	139.5	25.4	656	1	LSHR_PIG
9	139	25.3	925	1	GLHR_AMEL
10	138.5	25.2	366	1	LSHR_CHICK
11	138.5	25.2	676	1	LSHR_CALJA
12	138.5	25.2	699	1	LSHR_HUMAN
13	136.5	24.9	700	1	LSHR_RAT
14	132.5	24.1	693	1	LSHR_CHICK
15	132.5	24.1	700	1	LSHR_MOUSE
16	129	23.5	694	1	FSHR_HORSE
17	126	23.0	692	1	FSHR_MOUSE
18	126	23.0	695	1	FSHR_PIG
19	125	22.8	695	1	FSHR_BOVIN
20	125	22.8	695	1	FSHR_HUMAN
21	125	22.8	695	1	FSHR_SHEEP
22	124	22.6	326	1	AAIR_CAVPO
23	124	22.6	907	1	LGR5_MOUSE
24	123	22.4	326	1	AAIR_HUMAN
25	122	22.2	687	1	FSHR_EQUAS
26	122	22.2	692	1	FSHR_RAT
27	122	22.2	695	1	FSHR_MOUSE
28	122	22.0	324	1	AAIR_CHICK
29	120.5	21.9	317	1	AA3R_SHEEP
30	120.5	21.9	753	1	TSHR_BOVIN
31	120.5	21.9	764	1	TSHR_CANFA
32	120.5	21.9	764	1	TSHR_SHEEP
33	120	21.9	326	1	AAIR_MOUSE

34	120	21.9	326	1	AA1R_RAT	P25099	rattus norv
35	120	21.9	828	1	LGR6_HUMAN	O9hbx8	homo sapien
36	119.5	21.8	318	1	AA3R_HUMAN	P33765	homo sapien
37	119.5	21.8	764	1	TSHR_RAT	P16163	rattus norv
38	119	21.7	326	1	AA1R_CANFA	P11616	canis fami1
39	119	21.7	332	1	AA2B_MOUSE	O60614	mus musculu
40	118.5	21.6	314	1	AA3R_CANFA	O28309	canis fami1
41	118.5	21.6	764	1	TSHR_MOUSE	P47750	mus musculu
42	117.5	21.4	319	1	AA3R_RABIT	O02667	oryctolagus
43	117	21.3	326	1	AA1R_BOVIN	P28190	bos taurus
44	116	21.1	332	1	AA2B_RAT	P29276	rattus norv
45	115	20.9	332	1	AA2B_HUMAN	P29275	homo sapien

## ALIGNMENTS

RESULT 1	ID	SEQUENCE	STANDARD	PRT	754 AA.
LGR8_HUMAN	AC	Q8WDXD	15-JUN-2002 (Rel. 41, Created)		
LGR8_HUMAN	DT	15-JUN-2002 (Rel. 41, Last sequence update)			
LGR8_HUMAN	DR	15-JUN-2002 (Rel. 41, Last annotation update)			
LGR8_HUMAN	DE	Relaxin receptor 2 (Leucine-rich repeat-containing G protein-coupled receptor 8) (G protein-coupled receptor affecting testicular descent).			
LGR8_HUMAN	GN	LGR8 OR GREAT.			
LGR8_HUMAN	OS	Homo sapiens (Human).			
LGR8_HUMAN	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
LGR8_HUMAN	NC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
LGR8_HUMAN	NC	NCBI_Taxid=9606;			
LGR8_HUMAN	RA	SEQUENCE FROM N.A. AND MUTAGENESIS OF ASP-647.			
LGR8_HUMAN	RA	MEDLINE=21669315; PubMed=11809971;			
LGR8_HUMAN	RA	Hsu S.Y., Nakabayashi K., Nishi S., Kumagai J., Kudo M.,			
LGR8_HUMAN	RA	Sherwood O.D., Hsueh A.J.W.;			
LGR8_HUMAN	RT	"Activation of orphan receptors by the hormone relaxin.";			
LGR8_HUMAN	RL	Science 295:671-674 (2002).			
LGR8_HUMAN	RL	[21]			
LGR8_HUMAN	RP	SEQUENCE FROM N.A.			
LGR8_HUMAN	RA	Gorlov I.P., Kamat A., Jones E., Lamb D., Truong A., Bogatcheva N.,			
LGR8_HUMAN	RA	Bishop C.E., McElreavey K., Agoulunik A.I.;			
LGR8_HUMAN	RT	"Mutations of the GREAT gene cause cryptorchidism.";			
LGR8_HUMAN	RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.			
LGR8_HUMAN	CC	-1- FUNCTION: Receptor for relaxin. The activity of this receptor is mediated by G proteins leading to stimulation of adenylate cyclase and an increase of cAMP. May also be a receptor for Leydig			
LGR8_HUMAN	CC	insulin-like peptide (INSL3).			
LGR8_HUMAN	CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
LGR8_HUMAN	CC	testis, thyroid, uterus, peripheral blood cells and bone marrow.			
LGR8_HUMAN	CC	-1- DISEASE: Defects in LGR8 seems to be a cause of impaired testicular descent (known as cryptorchidism). It is one of the most frequent congenital abnormalities in humans, involving 2-5% of male births. Cryptorchidism is associated with increased risk of infertility and testicular cancer.			
LGR8_HUMAN	CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
LGR8_HUMAN	CC	-1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.			
LGR8_HUMAN	CC	-1- CAUTION: It is uncertain whether Met-1 or Met-18 is the initiator.			
LGR8_HUMAN	CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
LGR8_HUMAN	CC	EMBL: AF403384; AAI69324.2; -			
LGR8_HUMAN	DR	EMBL: AF453828; AAL73946.1; -			
LGR8_HUMAN	DR	MIM: 606655; -			
LGR8_HUMAN	DR	MIM: 219050; -			

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DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003591; LRR_tyr.
DR Pfam: PF000001; 7tm1.1; 1.
DR Pfam: PF00057; ldl_recept_a; 1.
DR Pfam: PF00560; LRR; 8.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00192; LDLA; 1.
DR SMART: SM00369; LRR_TYP; 10.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL1; FALSE_NEG.
DR PROSITE: PS01209; LDLRA_1; 1.
DR PROSITE: PS00068; LDLRA_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Repeat;
KW Leucine-rich repeat.
FT DOMAIN 1 416 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1 417 437 1 (POTENTIAL).
FT DOMAIN 1 438 455 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 436 476 2 (POTENTIAL).
FT DOMAIN 477 507 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 529 537 3 (POTENTIAL).
FT TRANSMEM 538 558 4 (POTENTIAL).
FT TRANSMEM 559 592 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 593 613 5 (POTENTIAL).
FT TRANSMEM 614 639 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 640 660 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 661 673 6 (POTENTIAL).
FT TRANSMEM 674 694 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 695 754 7 (POTENTIAL).
FT DOMAIN 4 81 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 136 159 LDL-RECEPTOR CLASS A.
FT REPEAT 161 183 LRR 1.
FT REPEAT 184 207 LRR 2.
FT REPEAT 209 231 LRR 3.
FT REPEAT 233 255 LRR 4.
FT REPEAT 256 279 LRR 5.
FT REPEAT 281 303 LRR 6.
FT REPEAT 304 327 LRR 7.
FT REPEAT 329 351 LRR 8.
FT REPEAT 352 375 LRR 9.
FT DISULFID 495 573 LRR 10.
FT CARBOHYD 54 54 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 647 647 D->Y: LEADS TO CONSTITUTIVE INCREASE OF
BASAL CAMP.
SQ SEQUENCE 754 AA; 86452 MW; 2088ECD204C6A6C5 CRC64;
Query Match 100.0%; Score 549; DB 1; Length 754;
Best Local Similarity 100.0%; Pred. No. 3.4e-45;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DE Relaxin receptor 2 (leucine-rich repeat-containing G protein-coupled
DE receptor 8) (G protein-coupled receptor affecting testicular descent)
DE (G protein-coupled receptor 106).
DE LGR8 OR GREAT OR GPR106.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=21250990; PubMed=11353515;
RA Overbeek P.A., Gotlov I.P., Sutherland R.W., Houston J.B.,
RA Harrison W.R., Boettger-Tong H.L., Bishop C.E., Aguilnik A.I.;
RA "A transgenic insertion causing cryptorchidism in mice.";
RA Genesis 30:26-35(2001).
CC -!- FUNCTION: Receptor for relaxin. The activity of this receptor is
CC mediated by G proteins leading to stimulation of adenylate cyclase
CC and an increase of cAMP. May also be a receptor for Leydig
CC insulin-like peptide (INSL3) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in embryonic and adult gonads of
CC males and females, as well in male gubernaculum. Expressed also
CC in brain. Not detected in kidney, spleen and heart.
CC -!- DISEASE: Defects in LGR8 seems to be a cause of impaired
CC testicular descent (known as cryptorchidism).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
CC -!- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
CC -!- MISCELLANEOUS: By homology with the human sequence, it is
CC uncertain whether Met-1 is the initiator.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF346501; AL08943.1; -.
CC MGD: MGI:2153463; Gpr106.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003591; LRR_tyr.
DR Pfam: PF000001; 7tm1.1; 1.
DR Pfam: PF00057; ldl_recept_a; 1.
DR Pfam: PF00560; LRR; 8.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_FL2; 1.
DR PROSITE: PS01209; LDLRA_1; 1.
DR PROSITE: PS00068; LDLRA_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Repeat;
KW Leucine-rich repeat.
FT DOMAIN 1 399 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 400 420 1 (POTENTIAL).
FT DOMAIN 421 438 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 439 459 2 (POTENTIAL).
FT DOMAIN 460 490 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 491 511 3 (POTENTIAL).
FT DOMAIN 512 520 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 521 541 4 (POTENTIAL).
FT DOMAIN 542 575 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 576 596 5 (POTENTIAL).
FT TRANSMEM 597 622 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 623 643 6 (POTENTIAL).
FT DOMAIN 644 664 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 665 685 7 (POTENTIAL).
FT DOMAIN 686 737 CYTOPLASMIC (POTENTIAL).
FT REPEAT 119 142 LDL-RECEPTOR CLASS A.
FT REPEAT 144 166 LRR 1.

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FT	REPEAT	167	190	LRR 3:
FT <th>REPEAT</th> <td>192</td> <td>214</td> <th>LRR 4:</th>	REPEAT	192	214	LRR 4:
FT <th>REPEAT</th> <td>215</td> <td>238</td> <th>LRR 5:</th>	REPEAT	215	238	LRR 5:
FT <th>REPEAT</th> <td>239</td> <td>262</td> <th>LRR 6:</th>	REPEAT	239	262	LRR 6:
FT <th>REPEAT</th> <td>263</td> <td>286</td> <th>LRR 7:</th>	REPEAT	263	286	LRR 7:
FT <th>REPEAT</th> <td>287</td> <td>310</td> <th>LRR 8:</th>	REPEAT	287	310	LRR 8:
FT <th>REPEAT</th> <td>312</td> <td>334</td> <th>LRR 9:</th>	REPEAT	312	334	LRR 9:
FT <th>REPEAT</th> <td>335</td> <td>358</td> <th>LRR 10:</th>	REPEAT	335	358	LRR 10:
FT <th>DISULFID</th> <td>478</td> <td>556</td> <th>BY SIMILARITY.</th>	DISULFID	478	556	BY SIMILARITY.
FT <th>CARBOHYD</th> <td>37</td> <td>37</td> <th>N-LINKED (GLCNAC. . .) (POTENTIAL).</th>	CARBOHYD	37	37	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>121</td> <td>121</td> <th>N-LINKED (GLCNAC. . .) (POTENTIAL).</th>	CARBOHYD	121	121	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>257</td> <td>257</td> <th>N-LINKED (GLCNAC. . .) (POTENTIAL).</th>	CARBOHYD	257	257	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>318</td> <td>318</td> <th>N-LINKED (GLCNAC. . .) (POTENTIAL).</th>	CARBOHYD	318	318	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>350</td> <td>350</td> <th>N-LINKED (GLCNAC. . .) (POTENTIAL).</th>	CARBOHYD	350	350	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>361</td> <td>361</td> <th>N-LINKED (GLCNAC. . .) (POTENTIAL).</th>	CARBOHYD	361	361	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ <th>SEQUENCE</th> <td>737 AA:</td> <td>82943 MW;</td> <td>AF06535EALACE49 CR664;</td>	SEQUENCE	737 AA:	82943 MW;	AF06535EALACE49 CR664;
Query Match				
Best Local Similarity		87.1%;	Score 478;	DB 1; Length 737;
Matches 92; Conservative		86.0%;	Pred. No. 1.9e-38;	
		8;	Mismatches 7;	Indels 0; Gaps 0;
OY	1 GVNLIAFLIVSYFTMCSIOKTLQTTTEVNCNGREYAVANREFEYFSAICMIPVF 60			
Db	579 GNNLAFIVIAISYTMFCSHIKTLQTAEVSHSGKEVAAANREFEYSDAICMIPVF 638			
OY	61 VKILSLFRVELPDTMTSMIVIFFPLPVNSALNPILYTLTTFNFKDL 107			
Db	639 VKILSLQVEIPIGRITTSIMIVYEFPLPVNSALNPILYTLTTFNFKDL 685			
RESULT 3				
LGR7_HUMAN	STANDARD; PRT; 757 AA.			
AC	Q9HBJ9;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Relaxin receptor 1 (Leucine-rich repeat-containing G protein-coupled receptor 7).			
GN	LGR7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId:9606;			
RN	[1]			
RX	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND MUTAGENESIS OF ASP-637.			
RA	MEDLINE=20388592; PubMed=10935549;			
RA	Hsu S.Y., Kudo M., Chen T., Nakabayashi K., Bhalla A.,			
RA	van der Spek P.J., Van Duijn M., Hsueh A.J.W.;			
RT	"The three subfamilies of leucine-rich repeat-containing G protein-			
RT	coupled receptors (LGR): identification of LGR6 and LGR7 and the			
RT	signaling mechanism for LGR7."			
RL	Mol. Endocrinol. 14:1257-1271(2000).			
RN	[2]			
RP	CHARACTERIZATION.			
RX	PubMed=11517286;			
RA	Bartsch O., Bartlick B., Iyell R.;			
RT	"Relaxin signalling links tyrosine phosphorylation to			
RT	phosphodiesterase and adenyllyl cyclase activity."			
RL	Mol. Hum. Reprod. 7:799-809(2001).			
CC	-1- FUNCTION: Receptor for relaxin. The activity of this receptor is			
CC	mediated by G proteins leading to stimulation of adenylate cyclase			
CC	and an increase of cAMP. Binding of the ligand may also			
CC	activate a tyrosine kinase pathway that inhibits the activity of a			
CC	phosphodiesterase that degrades cAMP.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are			
CC	produced by alternative splicing.			
CC	-1- TISSUE SPECIFICITY: Expressed in the brain, kidney, testis,			
CC	placenta, uterus, ovary, adrenal, prostate, skin and heart. Not			
CC	detected in spleen.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.			

Query Match	SEQUENCE	757 AA:	86992 MW:	80798DBF3A3EF21 CRC64:	68.5%: Score 376; DB 1; Length 757;
CC	1-1 SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).				
CC	-----				
CC	CC This SWISS-PROT entry is copyright. It is produced through a collabora				
CC	CC between the Swiss Institute of Bioinformatics and the EMBL outstacis c				
CC	CC the European Bioinformatics Institute. There are no restrictions c				
CC	CC use by non-profit institutions as long as its content is in n				
CC	CC modified and this statement is not removed. Usage by and for comm				
CC	CC entitles requires a license agreement (See <a href="http://www.isb-sib.ch/ann">http://www.isb-sib.ch/ann</a>				
CC	CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL: AF190500; AAG17167.1; -				
DR	MI: 606654; -				
DR	HSP, P01130; 1LDR.				
DR	InterPro: IPR000217; GPCR_Rhodpsn.				
DR	InterPro: IPR002172; LDL_recept_A.				
DR	InterPro: IPR001611; LRR.				
DR	InterPro: IPR000372; LRR_Nterm.				
DR	InterPro: IPR003592; LRR_out.				
DR	InterPro: IPR003591; LRR_tyr.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	Pfam: PF00057; Idl_recept_a; 1.				
DR	Pfam: PF00560; LRR; 8.				
DR	PRINTS: PR00237; GPCR_HODOPSIN.				
DR	SMART: SM00192; LDLa; 1.				
DR	SMART: SM00370; LRR; 7.				
DR	SMART: SM00013; LRRNT; 1.				
DR	SMART: SM00369; LRR_TYP; 10.				
DR	PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.				
DR	PROSITE: PS02623; G-PROTEIN_RECEP_F1_2; 1.				
DR	PROSITE: PS01209; LDLRA_1; 1.				
DR	PROSITE: PS00668; LDLRA_2; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Repeat;				
KW	Leucine-rich repeat; Alternative splicing.				
FT	DOMAIN 1 409				
FT	TRANSMEM 410 430				
FT	DOMAIN 431 443				
FT	TRANSMEM 444 464				
FT	DOMAIN 465 486				
FT	TRANSMEM 487 507				
FT	DOMAIN 508 527				
FT	TRANSMEM 528 548				
FT	DOMAIN 549 577				
FT	TRANSMEM 578 598				
FT	DOMAIN 599 629				
FT	TRANSMEM 630 650				
FT	DOMAIN 651 651				
FT	TRANSMEM 652 672				
FT	DOMAIN 673 757				
FT	DOMAIN 26 63				
FT	REPEAT 125 148				
FT	REPEAT 150 172				
FT	REPEAT 173 196				
FT	REPEAT 198 220				
FT	REPEAT 221 244				
FT	REPEAT 245 269				
FT	REPEAT 270 293				
FT	REPEAT 294 317				
FT	REPEAT 319 341				
FT	REPEAT 343 365				
FT	DISULFID 485 563				
FT	CARBOHYD 36 36				
FT	CARBOHYD 127 127				
FT	CARBOHYD 264 264				
FT	CARBOHYD 272 272				
FT	CARBOHYD 325 325				
FT	CARBOHYD 368 368				
FT	VARSPLIC 63 96				
FT	MUTAGEN 637 637				
FT	SEQUENCE 757 AA: 86992 MW: 80798DBF3A3EF21 CRC64:				
FT					

[illegible][illegible]



RL FEBS Lett. 284:155-160(1991).  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RX TISSUE-Brain:  
 RA MEDLINE-96196578; PubMed-8612733;  
 RA Sajjadi F.G., Boyle D.L., Domingo R.C., Firestein G.S.;  
 RT "cDNA cloning and characterization of A31, an alternatively spliced  
 RT rat A3 adenosine receptor variant.";  
 RL FEBS Lett. 382:125-129(1996).  
 CC -1- FUNCTION: RECEPTOR FOR ADENOSINE. THE ACTIVITY OF THIS RECEPTOR  
 CC IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYL CYCLASE.  
 CC POSSIBLE ROLE IN REPRODUCTION.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: TESTIS, PARTICULARLY IN SPERMATOCYTES AND  
 CC SPERMATIDS BUT NOT IN SPERMATOGENIA. LOW LEVELS IN THE BRAIN.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING SPERMIOGENESIS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: X59249; CAA41937.1; -;  
 DR EMBL: M94152; AAA40680.1; -;  
 DR EMBL: X93219; CAA63702.1; -;  
 DR PIR: S17177; S17177.  
 DR PIR: A46152; A46152.  
 DR HSSP: P29274; IMH.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1.1.  
 DR PRINTS: PR00237; GPCRHOPOPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECPT\_FL\_1; 1.  
 DR PROSITE: PS0262; G-PROTEIN\_RECPT\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 16  
 FT TRANSMEM 17 39  
 FT DOMAIN 40 50  
 FT TRANSMEM 51 74  
 FT DOMAIN 75 86  
 FT TRANSMEM 87 108  
 FT DOMAIN 109 128  
 FT TRANSMEM 129 150  
 FT DOMAIN 151 179  
 FT TRANSMEM 180 200  
 FT DOMAIN 201 233  
 FT TRANSMEM 234 257  
 FT DOMAIN 258 263  
 FT TRANSMEM 264 286  
 FT DOMAIN 287 320  
 FT CARBOHYD 4  
 FT CARBOHYD 5  
 FT CARBOHYD 4  
 FT DISULFID 85  
 FT LIPID 305  
 FT VARSPLIC 305  
 FT CONFLICT 18  
 FT CONFLICT 68  
 FT CONFLICT 74  
 FT CONFLICT 132  
 FT CONFLICT 172  
 FT CONFLICT 288  
 FT CONFLICT 291  
 FT SIGNAL 295  
 SO SEQUENCE 320 AA; 36629 MW; 59DBA40C594ACDAB CRC64;  
 Query Match 26.5%; Score 145.5; DB 1; Length 320;  
 Best Local Similarity 29.2%; Pred. No. 4.4e-08;  
 Matches 31; Conservative 23; Mismatches 47; Indels 5; Gaps 2;

QY 4 LEAFILVSYITMFCSTOKTALQT----TEVRNCGREAVANRFFLVSDAICWIPV 59  
 DB 189 LPIVVMCTIYDIFYIINKLSQNLGTGRETRAFYAGREFYAKSLFLVFLPACIMPL 248  
 QY 60 FVFKILSLFRVEIPDTMSWIVIFFLPVNSALNPILYITLTTFEFD 105  
 DB 249 STINEVSEFNKPIE-IAMCIGILLSHANSMMNPYVACKIRKFE 293  
 RESULT 7  
 LSHR\_BOVIN  
 ID LSHR\_BOVIN STANDARD: PRT; 701 AA.  
 AC Q28005; P79133;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)  
 DE (LH-R) (lutinizizing hormone receptor).  
 GN LHGR.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxId=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Holstein; TISSUE-Ovary, and Testis;  
 RA Lusier J.G., Houde A., Ethier J., Silversides D.W.;  
 RL Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 80-701 FROM N.A.  
 RX MEDLINE-98193601; PubMed-9532424;  
 RA Mamlik R., Wolfenson D., Meidan R.;  
 RT "LH receptor mRNA and cytochrome P450 side-chain cleavage expression  
 RT in bovine theca and granulosa cells luteinized by LH or forskolin.";  
 RL Domest. Anim. Endocrinol. 15:103-114(1998).  
 CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGNADOTROPIC HORMONE.  
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
 CC ACTIVATE ADENYLATE CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC FSH/LSH/TSH SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 6 LEOICINE-RICH REPEATS (LRR).  
 CC -----  
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 CC -----  
 DR EMBL: U20504; AAC24012.1; -;  
 DR EMBL: U87230; AAC33486.1; -;  
 DR HSSP: P28888; ILDT.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR Pfam: PF00001; 7tm.1.1.  
 DR Pfam: PF00560; LRR; 2.  
 DR SMART: SMO0013; LRRNT; 1.  
 DR PROSITE: PS00237; G-PROTEIN\_RECPT\_FL\_1; 1.  
 DR PROSITE: PS0262; G-PROTEIN\_RECPT\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing.  
 FT SIGNAL 1 26  
 FT CHAIN 27 701  
 FT DOMAIN 27 365  
 FT TRANSMEM 366 387  
 FT EXTRACELLULAR (POTENTIAL).  
 FT RECEPTOR.  
 FT 1 (POTENTIAL).

FT DOMAIN 388 397 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 398 418 2 (POTENTIAL).  
 FT DOMAIN 419 441 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 442 464 3 (POTENTIAL).  
 FT DOMAIN 465 484 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 485 507 4 (POTENTIAL).  
 FT DOMAIN 508 527 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 528 551 5 (POTENTIAL).  
 FT DOMAIN 552 572 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 573 596 6 (POTENTIAL).  
 FT DOMAIN 597 607 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 608 629 7 (POTENTIAL).  
 FT DOMAIN 630 701 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 50 73 LRR 1.  
 FT REPEAT 124 149 LRR 2.  
 FT REPEAT 151 173 LRR 3.  
 FT REPEAT 174 198 LRR 4.  
 FT REPEAT 200 222 LRR 5.  
 FT REPEAT 223 246 LRR 6.  
 FT DISULFID 441 516 BY SIMILARITY.  
 FT CARBOHYD 101 176 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 176 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 197 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 301 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 315 291 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPPLIC 229 557 MISSING (IN SHORT ISOFORM).  
 FT CONFLICT 557 577 N -> D (IN REF. 2).  
 FT CONFLICT 577 589 I -> T (IN REF. 2).  
 FT CONFLICT 589 597 F -> S (IN REF. 2).  
 SQ SEQUENCE 701 AA: 78455 MW: 8CDEE92F59EBBD7 CRC64:

Query Match Best Local Similarity 26.5%; Score 145.5; DB 1; Length 701;  
 Matches 31; Conservative 24; Mismatches 42; Indels 7; Gaps 2;

QY 2 VNLAFLIVSYITMFCSTOKTALQTEVRNCGREAVANRFFVPSDAICWIPVEV 61  
 DB 536 LNMVAFIICACYIKIYFAVONDELMT-----NKDTKIAKMAVLIFDFCMAPISF 589  
 QY 62 VKLSLPRVE-IPDYMSTNVIFFLEPVNSALNLTLYLTINFRK 104  
 DB 590 FAISAAFKVPLVTNSKLVLFYVNSCANDELYAIFTKAQ 633  
 RESULT 8  
 LSHR\_PIG STANDARD: PRT; 696 AA.  
 AC P16582;  
 DT 01-AUG-1990 (rel. 15, Created)  
 DT 01-AUG-1990 (rel. 15, Last sequence update)  
 DT 16-OCT-2001 (rel. 40, Last annotation update)  
 DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R) (LH-R) (Luteinizing hormone receptor).  
 GN LHCGR.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN RP  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=89332517; PubMed=2502844;  
 RA MEDLINE=89332517; PubMed=2502844;  
 RA Jollivet A., Gulochon-Mantel A., Sar S., Jallat B., Garnier J.,  
 RA Milgrom E.;  
 RA "Cloning and sequencing of porcine LH-hCG receptor cDNA: variants  
 RT lacking transmembrane domain.";  
 RL Science 245:525-528(1989).  
 CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.  
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
 CC ACTIVATE ADENYLATE CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: A (SHOWN HERE), B, C AND D; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC FSH/LSH/TSH SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).  
 CC -----  
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 CC -----  
 DR EMBL: M29525; AAA31062.1; -;  
 DR EMBL: M29526; AAA31063.1; -;  
 DR EMBL: M29527; AAA31064.1; -;  
 DR EMBL: M29528; AAA31065.1; -;  
 DR PIR: A41344; A41344.  
 DR PIR: B41344; B41344.  
 DR PIR: C41344; C41344.  
 DR PIR: D41344; D41344.  
 DR HSSP: P22886; ILUT.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR Pfam: PF00560; LRR\_2.  
 DR SMART: SM00013; LRRNT.1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECP\_F1\_1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECP\_F1\_2.1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; signal;  
 KW Phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing.  
 FT FT  
 FT CHAIN 1 27  
 FT SIGNL 28 696  
 FT  
 FT DOMAIN 28 358  
 FT TRANSMEM 359 386  
 FT DOMAIN 387 395  
 FT TRANSMEM 396 418  
 FT DOMAIN 419 439  
 FT TRANSMEM 440 462  
 FT DOMAIN 463 482  
 FT TRANSMEM 483 505  
 FT TRANSMEM 506 525  
 FT TRANSMEM 526 547  
 FT TRANSMEM 548 570  
 FT TRANSMEM 571 594  
 FT TRANSMEM 595 605  
 FT TRANSMEM 606 626  
 FT TRANSMEM 627 696  
 FT DOMAIN 48 71  
 FT REPEAT 122 147  
 FT REPEAT 149 171  
 FT REPEAT 172 196  
 FT REPEAT 198 220  
 FT REPEAT 221 244  
 FT DISULFID 439 514  
 FT CARBOHYD 99 99  
 FT CARBOHYD 174 174  
 FT CARBOHYD 195 195  
 FT CARBOHYD 291 291  
 FT CARBOHYD 299 299  
 FT CARBOHYD 313 313  
 FT VARSPPLIC 317 329  
 FT  
 FT VARSPPLIC 330 696  
 FT VARSPPLIC 317 331  
 FT  
 FT VARSPPLIC 332 696  
 FT VARSPPLIC 317 628  
 FT  
 FT VARSPPLIC 696 AA: 78092 MW: 593DEF1C25F92FE CRC64:

Query Match

25.4%; Score 139.5; DB 1; Length 696;

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FT TRANSMEM 740 763 6 (POTENTIAL) .
FT DOMAIN 740 764 7 EXTRACELLULAR (POTENTIAL) .
FT TRANSMEM 775 795 7 (POTENTIAL)
FT TRANSMEM 796 925 5 CYTOSOLIC (POTENTIAL)
FT DOMAIN 333 461 5 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 333 349 1 (INCOMPLETE) .
FT REPEAT 350 384 2.
FT REPEAT 385 419 3.
FT REPEAT 420 453 4.
FT REPEAT 454 461 5 (INCOMPLETE) .
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT VARSPLIC 235 925 MISSING (IN SHORT ISOFORM) .
SQ SEQUENCE 925 AA; 100059 MW; D03A256368452FBD CRC64;

Query Match 25.3%; Score 139; DB 1; Length 925;
Best Local Similarity 29.6%; Pred. No. 4.7e-06;
Matches 32; Conservative 24; Mismatches 46; Indels 6; Gaps 3;

QY 2 VNLLAFLLVSYITM-PCSIQKALQNTVEVNCNGREVAANRPFVSPDAICWV 60
DB 700 VNGSFSIVMLISMLYVYVSGDMECAPKRN----DSKVAKRMAIIYTDMLCWAPLA 755
QY 61 VKLTLSF-RVEIPDTMTSWIVIFELPVNSALNPILYLTNTNFQDKL 107
DB 756 FEGLLAARGQFLTLVYQSKILLVFEPFINSICNPFLVAFKAFKREL 803

RESULT 10
LSHR_CHICK ID LSHR_CHICK STANDARD; PRT; 366 AA.
AC Q96074;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin-choriogonadotropic hormone receptor (LH/CG-R) (LSH-R)
DE (luteinizing hormone receptor) (fragment).
GN LHCGR.
OS Gallus gallus (Chicken) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96426554; PubMed=8828833;
RA Johnson A.L., Bridgham J.T., Wagner B.;
RT "Characterization of a chicken luteinizing hormone receptor (LH-R)
RT complementary deoxyribonucleic acid, and expression of cLH-R
RT messenger ribonucleic acid in the ovary.";
RL Biol. Reprod. 55:304-309(1996).
-1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
-1- THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYLYLATE CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC FSH/LSH/TSH SUBFAMILY.
CC -----
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CC -----
DR EMBL: U31987; AAC59907.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.

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DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Phosphorylation.

FT NON\_TER 1 1  
 FT DOMAIN <1 26  
 FT TRANSMEM 27 48  
 FT DOMAIN 49 58  
 FT TRANSMEM 59 79  
 FT DOMAIN 80 102  
 FT TRANSMEM 103 125  
 FT DOMAIN 126 145  
 FT TRANSMEM 146 168  
 FT DOMAIN 169 188  
 FT TRANSMEM 189 212  
 FT DOMAIN 213 233  
 FT TRANSMEM 234 257  
 FT DOMAIN 258 268  
 FT TRANSMEM 269 290  
 FT DOMAIN 291 366  
 FT DISULFID 102 177  
 SQ SEQUENCE 366 AA; 40759 MW; C2F199F9E3CBCCA CRC64;

Query Match 25.2%; Score 138.5; DB 1; Length 366;  
 Best Local Similarity 28.8%; Pred. No. 2.3e-06;  
 Matches 30; Conservative 23; Mismatches 44; Indels 7; Gaps 2;

OY 2 VNLAFLIIVSYITMPCSIQKTAQTTEVRNCGREAVANRFFVFSDAICWIPFV 61  
 DB 197 LVNIAFLVLCACIKYIKYIAVQNPVLAA-----NKDTKIAKMAILLFDTCMAPISF 250

OY 62 VKILSLERVE-IPDTMTSMIVIFPLVNSALNPLTYLTTFNFK 104  
 DB 251 FAISAAKMPILVTNISKVLIVLFYVNSCANPFLVAIFTKRQ 294

RESULT 11  
 LSHR\_CALJA STANDARD; PRT; 676 AA.

AC 002721;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)  
 DE (LSH-R) (Luteinizing hormone receptor).  
 GN LHGR.  
 OS Callitrix jacchus (Common marmoset).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;  
 OC Callitrix.  
 OX NCBI\_Taxid=9483;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE-Testis;  
 RX MEDLINE=97307697; PubMed=9165039;  
 RA Zhang F.-P., Rannikko A.S., Manna P.R., Fraser H.M., Huhtaniemi I.T.;  
 RT "Cloning and functional expression of the luteinizing hormone  
 RT receptor complementary deoxyribonucleic acid from the marmoset monkey  
 RT tests: absence of sequences encoding exon 10 in other species.";  
 RT Endocrinology 138:2481-2490(1997).  
 RL Endocrinology 138:2481-2490(1997).  
 CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.  
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
 CC ACTIVATE ADENYLATE CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC FSH/LSH/TSH SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 5 LEUCINE-RICH REPEATS (LRR).  
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DR EMBL; U80673; AAB53698.1; -.  
 DR HSSP; P22888; ILUT.  
 DR InterPro: IPR000276; GPCR Rhodopsin.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR Pfam; PF00360; LRR; 2.  
 DR SMART; SM00013; LRRNT; 1.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KM Phosphorylation; Repeat; Leucine-rich repeat.  
 FT SIGNAL 1 29  
 FT CHAIN 30 676  
 FT DOMAIN 30 340  
 FT TRANSMEM 341 362  
 FT DOMAIN 363 372  
 FT TRANSMEM 373 392  
 FT DOMAIN 394 416  
 FT TRANSMEM 417 439  
 FT DOMAIN 440 459  
 FT TRANSMEM 460 482  
 FT DOMAIN 483 502  
 FT TRANSMEM 503 526  
 FT DOMAIN 527 547  
 FT TRANSMEM 548 571  
 FT DOMAIN 572 582  
 FT TRANSMEM 583 604  
 FT DOMAIN 605 676  
 FT REPEAT 52 75  
 FT REPEAT 126 151  
 FT REPEAT 153 175  
 FT REPEAT 176 200  
 FT REPEAT 225 248  
 FT DISULFID 416 491  
 FT CARBOHYD 103 103  
 FT CARBOHYD 178 178  
 FT CARBOHYD 199 199  
 SQ SEQUENCE 676 AA; 75677 MW; FB018227641654E1 CRC64;

Query Match 25.2%; Score 138.5; DB 1; Length 676;  
 Best Local Similarity 26.9%; Pred. No. 4e-06;  
 Matches 28; Conservative 27; Mismatches 42; Indels 7; Gaps 2;

OY 2 VNLAFLIIVSYITMPCSIQKTAQTTEVRNCGREAVANRFFVFSDAICWIPFV 61  
 DB 511 LVNVAFLIIVLCACIKYIKYIAVQNPVLAA-----NKDTKIAKMAILLFDTCMAPISF 564

OY 62 VKILSLERVE-IPDTMTSMIVIFPLVNSALNPLTYLTTFNFK 104  
 DB 565 FAISAAKMPILVTNISKVLIVLFYVNSCANPFLVAIFTKR 608

RESULT 12  
 LSHR\_HUMAN STANDARD; PRT; 699 AA.

AC P22888;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)  
 DE (LSH-R) (Luteinizing hormone receptor).  
 GN LHGR OR LHRHR OR LCGR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE-Ovary; PubMed-2244890;  
 RX MEDLINE-91058534; PubMed-2244890;  
 RA Minegishi T., Nakamura K., Takakura Y., Miyamoto K., Hasegawa Y.,  
 RT Ibuti Y., Igarashi M.;  
 RL "Cloning and sequencing of human LH/hCG receptor cDNA.";  
 RN Biochem. Biophys. Res. Commun. 172:1049-1054(1990).  
 RP [2]  
 RC SEQUENCE FROM N.A.  
 RX TISSUE-Ovary;  
 RA MEDLINE-92017881; PubMed-1922095;  
 RT Jia X.-C., Oikawa M., Bo M., Tanaka T., Ny T., Boime I., Hsueh A.J.W.;  
 RL "Expression of human luteinizing hormone (LH) receptor: interaction  
 with LH and chorionic gonadotropin from human but not equine, rat,  
 Mol. Endocrinol. 5:759-768(1991).  
 RP [3]  
 RC SEQUENCE FROM N.A.  
 RX TISSUE-Thyroid;  
 RA MEDLINE-91155962; PubMed-2293030;  
 RT Frazier A.L., Robbins L.S., Stork P.J., Sprengel R., Segaloff D.L.,  
 RA Cone R.D.;  
 RL "Isolation of TSH and LH/CG receptor cDNAs from human thyroid:  
 regulation by tissue specific splicing.";  
 RN Mol. Endocrinol. 4:1264-1276(1990).  
 RP [4]  
 RC 3D-STRUCTURE MODELING OF 51-232.  
 RX MEDLINE-96363672; PubMed-8747461;  
 RA Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H.,  
 RT Hendrickson W.A., el Tayar N.;  
 RL "Structural predictions for the ligand-binding region of glycoprotein  
 hormone receptors and the nature of hormone-receptor interactions.";  
 RN Structure 3:1141-1153(1995).  
 RP [5]  
 RC VARIANT FMPP GLY-578.  
 RX MEDLINE-94019815; PubMed-7692306;  
 RA Shenker A., Laue L., Kosugi S., Merendino J.J. Jr., Minegishi T.,  
 RT Cutler G.B. Jr.;  
 RL "A constitutively activating mutation of the luteinizing hormone  
 receptor in familial male precocious puberty.";  
 RN Nature 365:652-654(1993).  
 RP [6]  
 RC VARIANTS FMPP ILE-571 AND GLY-578.  
 RX MEDLINE-94108425; PubMed-8281137;  
 RA Kremer H., Mariman E., Otten B.J., Moll G.W. Jr., Stoelinga G.B.A.,  
 RT Wit J.M., Jansen M., Drop S.L., Paas B., Ropers H.-H., Brunner H.G.;  
 RL "Coregulation of missense mutations of the luteinizing hormone  
 receptor gene with familial male-limited precocious puberty.";  
 RN Hum. Mol. Genet. 2:1779-1783(1993).  
 RP [7]  
 RC VARIANT FMPP ILE-577.  
 RX MEDLINE-95276728; PubMed-7757065;  
 RA Kosugi S., van Dop C., Geffner M.E., Rabi W., Carel J.-C.,  
 RT Chausain J.-L., Mori T., Merendino J.J. Jr., Shenker A.;  
 RL "Characterization of heterogeneous mutations causing constitutive  
 activation of the luteinizing hormone receptor in familial male  
 precocious puberty.";  
 RN Hum. Mol. Genet. 4:183-188(1995).  
 RP [8]  
 RC VARIANT FMPP VAL-572.  
 RX MEDLINE-95229804; PubMed-7714085;  
 RA Yano K., Saji M., Hidaka A., Moriya N., Okuno A., Kohn L.D.,  
 RT Cutler G.B. Jr.;  
 RL "A new constitutively activating point mutation in the luteinizing  
 hormone/choriogonadotropin receptor gene in cases of male-limited  
 precocious puberty.";  
 RN J. Clin. Endocrinol. Metab. 80:1162-1168(1995).  
 RP [9]  
 RC VARIANT FMPP VAL-568.  
 RX MEDLINE-95355560; PubMed-7629248;  
 RA Latronico A.C., Anastasi J., Arnold I.J., Mendonca B.B., Domenice S.,  
 RT Albano M.C., Zachman K., Wajchenberg B.L., Tsigos C.;  
 RL "A novel mutation of the luteinizing hormone receptor gene causing  
 male gonadotropin-independent precocious puberty.";

RL J. Clin. Endocrinol. Metab. 80:2490-2494(1995).  
 RN [10]  
 RC VARIANT ICH PRO-593.  
 RX MEDLINE-95235561; PubMed-7719343;  
 RA Kremer H., Kraaij R., Toledo S.P.A., Post M., Fridman J.B.,  
 RT Hayashida C.Y., van Reen M., Milgrom E., Ropers H.-H., Mariman E.,  
 RL Thermen A.P.N., Brunner H.G.;  
 RN "Male pseudohermaphroditism due to a homozygous missense mutation of  
 the luteinizing hormone receptor gene.";  
 RL Nat. Genet. 9:160-164(1995).  
 RP [11]  
 RC VARIANT FMPP ILE-577.  
 RX MEDLINE-96233936; PubMed-8829636;  
 RA Cocco S., Meloni A., Marini M.G., Cao A., Moi P.;  
 RT "A missense (T577T) mutation in the luteinizing hormone receptor gene  
 associated with familial male-limited precocious puberty.";  
 RL Hum. Mutat. 7:164-166(1996).  
 RN [12]  
 RC VARIANT FMPP THR-398.  
 RX MEDLINE-97083378; PubMed-8929952;  
 RA Evans B.A.J., Bowen D.J., Smith P.J., Clayton P.E., Gregory J.W.;  
 RT "A new point mutation in the luteinizing hormone receptor gene in  
 familial and sporadic male limited precocious puberty: genotype does  
 not always correlate with phenotype.";  
 RL J. Med. Genet. 33:143-147(1996).  
 RN [13]  
 RC VARIANT ICH TYR-616.  
 RX MEDLINE-96157015; PubMed-8559204;  
 RA Latronico A.C., Anastasi J., Arnold I.J., Rapaport R., Mendonca B.B.,  
 RT Bloise W., Castro M., Tsigos C., Chrousos G.P.;  
 RL "Brief report: testicular and ovarian resistance to luteinizing  
 hormone caused by inactivating mutations of the luteinizing  
 hormone-receptor gene.";  
 RN New Engl. J. Med. 334:507-512(1996).  
 RP [14]  
 RC VARIANT ICH ARG-131.  
 RX MEDLINE-97358168; PubMed-9215288;  
 RA Mistrati W., Meurt G., Fissard S., Bouvattier C., Beau I.,  
 RT Loosfelt H., Jollivet A., Rapaport R., Milgrom E., Bougneres P.;  
 RL "Comparison of immunocytochemical and molecular features with the  
 phenotype in a case of incomplete male pseudohermaphroditism  
 associated with a mutation of the luteinizing hormone receptor.";  
 RN J. Clin. Endocrinol. Metab. 82:2159-2165(1997).  
 RP [15]  
 RC VARIANTS LEU-GLN-13 INS; SER-284 AND ASN-306.  
 RX Wu S.-M., Jose M., Hallermeier K., Rennett O.M., Chan W.-Y.;  
 RT "Polymorphisms in the coding exons of the human luteinizing hormone  
 receptor gene.";  
 RL Hum. Mutat. 11:333-334(1998).  
 RN [16]  
 RC VARIANT FMPP VAL-373.  
 RX MEDLINE-98128689; PubMed-9467560;  
 RA Gronoill J., Partsch C.-J., Simoni M., Nordhoff V., Stippell W.G.,  
 RT Nieschlag E., Saxena B.B.;  
 RL "A mutation in the first transmembrane domain of the lutropin receptor  
 causes male precocious puberty.";  
 RN J. Clin. Endocrinol. Metab. 83:476-480(1998).  
 RP [17]  
 RC VARIANT ICH LYS-354.  
 RX MEDLINE-98289384; PubMed-9626144;  
 RA Stavrou S.S., Zhu Y.S., Cai L.O., Katz M.D., Herrera C.,  
 RT Defillo-Ricart M., Imperato-Mcginley J.;  
 RL "A novel mutation of the human luteinizing hormone receptor in 46XX  
 and 46XX sisters.";  
 RN J. Clin. Endocrinol. Metab. 83:2091-2098(1998).  
 RP [18]  
 RC VARIANT FMPP ARG-457.  
 RX MEDLINE-98326270; PubMed-9661624;  
 RA Latronico A.C., Abell A.N., Segaloff D.L., Mendonca B.B.;  
 RT Brito V.N., Billebeck A.E., Segaloff D.L., Mendonca B.B.;  
 RL "A unique constitutively activating mutation in third transmembrane  
 helix of luteinizing hormone receptor causes sporadic male  
 gonadotropin-independent precocious puberty.";

RL J. Clin. Endocrinol. Metab. 83:2435-2440(1998).  
 [19]  
 RN VARIANT LCH 608-LEU-VAL-609 DEL.  
 RP MEDLINE-98173094; PubMed-9514160;  
 RX Latorico A.C., Chai Y., Arnold I.J.P., Liu X., Mendonca B.B.,  
 RA Segaloff D.L.;  
 RA "A homozygous microdeletion in helix 7 of the luteinizing hormone  
 RT receptor associated with familial testicular and ovarian resistance is  
 RT due to both decreased cell surface expression and impaired effector  
 RT activation by the cell surface receptor."  
 RL Mol. Endocrinol. 12:442-450(1998).  
 RN [20]  
 RP VARIANT LCH LYS-625.  
 RX MEDLINE-98289955; PubMed-9626653;  
 RA Martens J.W., Verhoef-Post M., Abelin N., Ezabella M., Toledo S.P.,  
 RA Bruner H.G., Themmen A.P.;  
 RA "A homozygous mutation in the luteinizing hormone receptor causes  
 RT partial Leydig cell hypoplasia: correlation between receptor activity  
 RT and phenotype."  
 RL Mol. Endocrinol. 12:775-784(1998).  
 RN [21]  
 RP VARIANT LEYDIG CELL TUMOR HIS-578.  
 RX MEDLINE-20037768; PubMed-10580072;  
 RA Liu G., Duranceau L., Carel J.-C., Monroe J., Doyle D.A., Shenker A.;  
 RA "Leydig-cell tumors caused by an activating mutation of the gene  
 RT encoding the luteinizing hormone receptor."  
 RL New Engl. J. Med. 341:1731-1736(1999).  
 CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.  
 CC -1- THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
 CC ACTIVATE ADENYLATE CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM (SHOWN  
 CC HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: GONADAL AND THYROID CELLS.  
 CC -1- DISEASE: DEFECTS IN LHCG ARE A CAUSE OF FAMILIAL MALE  
 CC PRECOXIOUS PUBERTY (FMP) (ALSO KNOWN AS TESTOTOXICOSIS). IN FMP  
 CC THE RECEPTOR IS CONSTITUTIVELY ACTIVATED.  
 CC -1- DISEASE: DEFECTS IN LHCG ARE A CAUSE OF LEYDIG CELL HYPOPLASIA;  
 CC (LCH) AN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY MALE  
 CC PSEUDOHERMAPHRODITISM. IN LCH THE TESTES ARE SMALL WITH MARKED  
 CC  
 Query Match 25.28; Score 138.5; DB 1; Length 699;  
 Best Local Similarity 27.9%; Pred. No. 4.1e-06;  
 Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;  
 QY 2 VNLAFLVITFSYITMFCSTOKTALQTEVRNCGREVANANFEVSDAICMIPFV 61  
 DB 534 LNVVAFITICACYIKIFYAVRNELAT-----NKDTKIAKMAIIFDTFCMADISF 587  
 QY 62 VKLISLFRVE-IDPTMTSMIVIFELPYNSALNPILYLTITNFR 104  
 DB 588 FALSAAFKVLITVNSKVLVLEFPINSCANPLVIAIFIKITQ 631  
 RESULT 13  
 LSHR\_RAT  
 ID LSHR\_RAT STANDARD: PRT: 700 AA.  
 AC P16235; P70646; Q63807; Q63808; Q63809;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Luteinizing hormone receptor precursor (LH/CG-R)  
 GN LHCGR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-89332512; PubMed-2502842;  
 RA McFarland K.C., Sprengel R., Phillips H.S., Koehler M.,  
 RA Rosenblit N., Nikolics K., Segaloff D.L., Seeburg P.H.;

RT "Luteinizing hormone receptor: an unusual member of the G  
 RT protein-coupled receptor family."  
 RL Science 245:494-499(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC STRAIN-Sprengel-Dawley; TISSUE-Ovary;  
 RX MEDLINE-92347604; PubMed-1353463;  
 RA Aatsinki J.T., Pietila E.M., Lakkakorpi J.T., Rajaniemi H.J.;  
 RT "Expression of the LH/CG receptor gene in rat ovarian tissue is  
 RT regulated by an extensive alternative splicing of the primary  
 RT transcript."  
 RL Mol. Cell. Endocrinol. 84:127-135(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91209270; PubMed-2019252;  
 RA Koo Y.B., Staughter R.G., Ji T.H.;  
 RT "Structure of the luteinizing hormone receptor gene and multiple  
 RT exons of the coding sequence."  
 RL Endocrinology 128:2297-2308(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE-9106819; PubMed-1976554;  
 RA Bernard M.P., Myers R.V., Moyle W.R.;  
 RT "Cloning of rat luteinizing hormone receptor analogs lacking the soybean  
 RT lectin domain."  
 RL Mol. Cell. Endocrinol. 71:R19-R23(1990).  
 RN [5]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE-91126285; PubMed-2281186;  
 RA Segaloff D.L., Sprengel R., Nikolics K., Ascoli M.;  
 RT "Structure of the luteinizing hormone receptor."  
 RL Recent Prog. Horm. Res. 46:261-303(1990).  
 RN [6]  
 RP SEQUENCE OF 295-700 FROM N.A.  
 RX MEDLINE-91060531; PubMed-2174034;  
 RA Tsai-Morris C.H., Buccio E., Wang W., Dufau M.L.;  
 RT "Intronic nature of the rat luteinizing hormone receptor gene defines  
 RT a soluble receptor subspecies with hormone binding activity."  
 RL J. Biol. Chem. 265:19385-19388(1990).  
 RN [7]  
 RP SEQUENCE OF 27-37.  
 RX MEDLINE-89174723; PubMed-2925659;  
 RA Roche P.C., Ryan R.J.;  
 RT "Purification, characterization, and amino-terminal sequence of rat  
 RT ovarian receptor for luteinizing hormone/human chorionadotropin."  
 RL J. Biol. Chem. 264:4636-4641(1989).  
 RN [8]  
 RP MOTAGENESIS.  
 RX MEDLINE-91332007; PubMed-1714448;  
 RA Ji T.H., Ji T.H.;  
 RT "Asp383 in the second transmembrane domain of the luteinizing hormone  
 RT is important for high affinity hormone binding and cAMP production."  
 RL J. Biol. Chem. 266:14953-14957(1991).  
 CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.  
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
 CC ACTIVATE ADENYLATE CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 11 ISOFORMS WHICH DIFFER IN  
 CC SUBCELLULAR LOCATION ARE PRODUCED BY ALTERNATIVE SPLICING  
 CC OF THE SAME GENE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC FSH/LSH/TSH SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).  
 CC  
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 CC  
 CC EMBL; M26199; AAA41528.1; -



RL Gene 197:121-127(1997).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=white leghorn;  
 RC MEDLINE=97057887; PubMed=8902217;  
 RA You S., Bridgman J.T., Foster D.N., Johnson A.L.;  
 RT "Characterization of the chicken follicle-stimulating hormone  
 RT receptor (cFSH-R) complementary deoxyribonucleic acid, and expression  
 RT of cFSH-R messenger ribonucleic acid in the ovary.";  
 RL Biol. Reprod. 55:1055-1062(1996).  
 CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY  
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
 CC ADENYLATE CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC FSH/LSH/TSH SUBFAMILY  
 CC -1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).  
 CC -----  
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 CC -----  
 DR EMBL: D87871; BAA13487.1; -;  
 DR EMBL: U51097; AAC60030.1; -;  
 DR HSSP: P23945; 1XUN.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR Pfam: PF00001; 7tm1.1;  
 DR Pfam: PF00560; LRR\_1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR SMART: SM0013; LRRNT; 1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECPT\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECPT\_F1\_2; 1.  
 KM G-protein coupled receptor: Transmembrane; Glycoprotein; Signal;  
 KV Phosphorylation; Repeat; Leucine-rich repeat.  
 FT SIGNAL 1  
 FT CHAIN 17  
 FT DOMAIN 18 693  
 FT TRANSMEM 18 366  
 FT DOMAIN 367 387  
 FT TRANSMEM 388 398  
 FT DOMAIN 399 421  
 FT TRANSMEM 422 443  
 FT DOMAIN 444 465  
 FT TRANSMEM 466 485  
 FT DOMAIN 486 508  
 FT TRANSMEM 509 528  
 FT DOMAIN 529 550  
 FT TRANSMEM 551 573  
 FT DOMAIN 574 597  
 FT TRANSMEM 598 608  
 FT DOMAIN 609 630  
 FT TRANSMEM 631 693  
 FT DOMAIN 693 693  
 FT REPEAT 45 68  
 FT REPEAT 69 93  
 FT REPEAT 95 118  
 FT REPEAT 119 143  
 FT REPEAT 168 192  
 FT REPEAT 193 216  
 FT REPEAT 218 240  
 FT DISULF 442 517  
 FT CARBOHD 47 47  
 FT CARBOHD 191 191  
 FT CARBOHD 199 199  
 FT CARBOHD 268 268  
 FT CONFLICT 4 4  
 FT CONFLICT 88 88  
 FT CONFLICT 140 140  
 FT CONFLICT 174 174

FT CONFLICT 191 191 N -> S (IN REF. 2).  
 FT CONFLICT 329 329 V -> L (IN REF. 2).  
 SQ SEQUENCE 693 AA, 78697 MW, 46F9869655A1BEC CRC64;  
 Query Match 24.1%; Score 132.5; DB 1; Length 693;  
 Best local similarity 27.9%; Pred. No. 1.5e-05;  
 Matches 29; Conservative 25; Mismatches 43; Indels 7; Gaps 2;  
 QY 2 VNLLAFLLVFSYIMFCISQKALQTTETVRNFGGEVAVANFFIVSDAICRPVY 61  
 DB 537 LNVLAFLVILICICICIFVIRNPVVIS-----NSDTKAKRMALIFDFLCMAPISE 590  
 QY 62 VKILSLFRVEIPDPTMTSMI-VIFELPVNSALNPILYLTFTNFK 104  
 DB 591 FALSASLRVPLIVSKSKILLVFPYFINSANFVLAIFTKTR 634  
 RESULT 15  
 LSHR\_MOUSE STANDARD; PRT; 700 AA.  
 AC P30730;  
 DT 01-APR-1993 (rel. 25, Created)  
 DT 01-APR-1993 (rel. 25, Last sequence update)  
 DT 16-OCT-2001 (rel. 40, Last annotation update)  
 DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)  
 DE (LSH-R) (lutelinizing hormone receptor).  
 GN LHCGR OR LHR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92165799; PubMed=1311310;  
 RX Gudermann T., Birnbaumer M., Birnbaumer L.;  
 RT "Evidence for dual coupling of the murine lutelinizing hormone  
 RT receptor to adenylyl cyclase and phosphoinositide breakdown and Ca2+  
 RT mobilization. Studies with the cloned murine lutelinizing hormone  
 RT receptor expressed in L cells.";  
 RL J. Biol. Chem. 267:4479-4488(1992).  
 RN [2]  
 RP SEQUENCE OF 1-58 FROM N.A.  
 RA MEDLINE=93093308; PubMed=1459341;  
 RX Huhnameni I.T., Eskola V., Pakarinen P., Matikainen T., Sprengel R.;  
 RT "The murine lutelinizing hormone and follicle-stimulating hormone  
 RT receptor genes: transcription initiation sites, putative promoter  
 RT sequences and promoter activity.";  
 RL Mol. Cell. Endocrinol. 88:55-66(1992).  
 CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.  
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
 CC ACTIVATE ADENYLATE CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC FSH/LSH/TSH SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 4 LEUCINE-RICH REPEATS (LRR).  
 CC -----  
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 CC -----  
 DR EMBL: S49753; AAB24402.1; -;  
 DR EMBL: M81310; AAA39432.1; -;  
 DR EMBL: M87571; AAA39433.1; -;  
 DR PIR: A42395; A42395.  
 DR HSSP: P22888; 1LUT.  
 DR MGD: MGI:96783; Lhgfr.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR\_Nterm.

DR Pfam; PF00001; 7tm\_1; 1.  
 DR Pfam; PF00560; LRR; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_FL1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECPT\_FL2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Phosphorylation; Repeat; Leucine-rich repeat.  
 FT SIGNAL 1 26  
 FT CHAIN 27 700  
 FT DOMAIN 27 362  
 FT TRANSMEM 363 390  
 FT DOMAIN 391 399  
 FT TRANSMEM 400 422  
 FT DOMAIN 423 443  
 FT TRANSMEM 444 466  
 FT DOMAIN 467 509  
 FT TRANSMEM 487 529  
 FT DOMAIN 510 551  
 FT TRANSMEM 530 551  
 FT DOMAIN 552 574  
 FT TRANSMEM 575 598  
 FT DOMAIN 599 609  
 FT TRANSMEM 610 631  
 FT DOMAIN 632 700  
 FT REPEAT 52 75  
 FT REPEAT 126 150  
 FT REPEAT 176 200  
 FT REPEAT 225 248  
 FT DISULFID 443 518  
 FT CARBOHYD 103 103  
 FT CARBOHYD 178 178  
 FT CARBOHYD 199 199  
 FT CARBOHYD 295 295  
 FT CARBOHYD 303 303  
 FT CARBOHYD 317 317  
 SO SEQUENCE 700 AA; 78214 MW; 8A6840A011E1E014 CRC64;

Query Match 24.1%; Score 132.5; DB 1; Length 700;  
 Best Local Similarity 26.9%; Pred. No. 1.5e-05;  
 Matches 28; Conservative 25; Mismatches 44; Indels 7; Gaps 2;

OY 2 VNLAFLLIVFSYIMFCSIOKTAQTQTEVRNCGREVAVANRFFIVPSDAICWIPYFV 61  
 DB 538 LNAVAFVVICACVRIYFAVQNPETAP-----NKDKRIAKKMAILITPDTCPAPISF 591  
 OY 62 VKLSLFVE-IPDTMTSMIVIFLPLVNSALNPILYTLTNFFK 104  
 DB 592 FAISAFKVPPLITVTNSKVLVLVFPVNSCANPFLYAVETKAFQ 635

Search completed: May 22, 2003, 12:45:32  
 Job time : 26 secs

GenCore version 5.1.4.p5.4578  
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# OM protein - protein search, using sw model

Run on: May 22, 2003, 12:42:05 ; Search time 84 Seconds  
(without alignments) 262.465 Million cell updates/sec

Title: US-09-930-312-2  
Perfect score: 549  
Sequence: 1 GVNLLAFILVFSITMFCSS.....NSALNPILYLTITNFKDKL 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

1: SPTRMBL\_21:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.phage:\*  
11: sp.plant:\*  
12: sp.rodent:\*  
13: sp.virus:\*  
14: sp.vertibrate:\*  
15: sp.unclassified:\*  
16: sp.virus:\*  
17: sp.bacteriophage:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	234	42.6	334	5	Q9VYG0	Q9VYG0 drosophila
2	225	41.0	359	5	Q9VBP0	Q9VBP0 drosophila
3	158	28.8	1012	5	Q95YI6	Q95YI6 asterina pe
4	158	28.8	1280	5	Q95YI7	Q95YI7 asterina pe
5	145.5	26.5	701	6	Q8SPS8	Q8SPS8 bos taurus
6	142	25.9	1050	6	Q9NM18	Q9NM18 drosophila
7	142	25.9	1300	5	Q9NKD6	Q9NKD6 drosophila
8	142	25.9	1360	5	Q9NDI1	Q9NDI1 drosophila
9	138.5	25.2	601	13	Q42500	Q42500 meleagris g
10	138.5	25.2	693	13	Q9DGC5	Q9DGC5 oreochromis
11	138.5	25.2	699	4	Q159G6	Q159G6 homo sapien
12	138.5	25.2	701	4	Q14751	Q14751 homo sapien
13	136.5	24.9	335	6	Q46387	Q46387 mustela vis
14	135.5	24.7	814	13	Q91949	Q91949 oncorhynch
15	134.5	24.5	793	13	Q91948	Q91948 oncorhynch
16	132.5	24.1	658	13	Q9PVN9	Q9PVN9 oncorhynch

17	131.5	24.0	293	6	Q95MF7	Q95MF7 canis fami
18	131.5	24.0	724	13	Q9VPV0	Q9VPV0 oncorhynch
19	128.5	23.4	779	13	Q91BN7	Q91BN7 morone saxa
20	127.5	23.2	696	13	Q98T85	Q98T85 ictalurus p
21	126.5	23.0	763	6	Q9BGN4	Q9BGN4 felis silve
22	126.5	23.0	778	13	Q98TF4	Q98TF4 oreochromis
23	126	23.0	829	5	Q9VEG4	Q9VEG4 drosophila
24	126	23.0	831	5	Q94979	Q94979 drosophila
25	126	23.0	831	5	Q8SX01	Q8SX01 drosophila
26	125.5	22.9	696	13	Q9DGF5	Q9DGF5 cynops pyr
27	125	22.8	410	4	Q16225	Q16225 homo sapien
28	124	22.6	459	11	Q8R301	Q8R301 mus musculu
29	123	22.4	326	4	Q8TAM8	Q8TAM8 homo sapien
30	123	22.4	695	13	Q8R428	Q8R428 cavia porce
31	123	22.2	701	13	Q9DGC6	Q9DGC6 oreochromis
32	122	22.2	688	11	Q64183	Q64183 ratu
33	121	22.0	326	11	Q08766	Q08766 mus musculu
34	120	21.9	310	11	Q8R0M5	Q8R0M5 mus musculu
35	120	21.9	928	4	Q9BYD7	Q9BYD7 homo sapien
36	119.5	21.8	470	4	Q43200	Q43200 homo sapien
37	119.5	21.8	533	4	Q9PIV4	Q9PIV4 homo sapien
38	118.5	21.6	319	6	Q9N1U0	Q9N1U0 oryctolagus
39	118.5	21.6	662	13	Q9PW16	Q9PW16 claria gar
40	118.5	21.6	764	11	Q9D697	Q9D697 mus musculu
41	117.5	21.4	739	6	Q9BGS5	Q9BGS5 sus scrofa
42	117.5	21.4	764	6	Q9BGS6	Q9BGS6 sus scrofa
43	117.5	21.4	764	6	Q8SP9	Q8SP9 sus scrofa
44	116.5	21.2	662	13	Q98T84	Q98T84 ictalurus p
45	116	21.1	107	11	Q99P16	Q99P16 mus musculu

## ALIGNMENTS

RESULT 1	ID	Q9VYG0	PRELIMINARY	PRT	334 AA.
AC	Q9VYG0				
DT	01-MAY-2000	(TREMBLrel. 13, Created)			
DE	01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DE	01-JUN-2001	(TREMBLrel. 17, Last annotation update)			
GN	CG4187	protein.			
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	SEQUENCE FROM N.A.				
RC	SPRAIN-BERKELEY;				
RX	MEDLINE-20196006; PubMed-10731132;				
RA	Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,				
RA	Abail J.F., Agbayani A., An H.-J., Andrews-Plankoch C., Baldwin D.,				
RA	Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,				
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,				
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,				
RA	Glock A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,				
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				

RA Lisko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,  
RA Palazolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Styrbas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.W., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
DR EMBL; AE003491; AAF4837.1; -;  
DR FLYBase; FBgn0030458; CG4187.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR001901; SecE.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PROSITE; PSS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
DR PROSITE; PSS01067; SEC\_E-SEC6M; UNKNOW\_1.  
DR PROSITE; PSS01067; SEC\_E-SEC6M; UNKNOW\_1.  
QJ SEQUENCE 334 AA; 37020 MW; 1662F2D467534061 CRC64;

Query Match	42.68;	Score 234;	DB 5;	Length 334;
Best Local Similarity	45.48;	Pred. No. 1.4e-13;		
Matches 49;	Conservative 20;	Mismatches 33;	Indels 6;	Gaps 2

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0y 2 VNLAEFLIVSYIMECSIQKT--AQTTEVANCFGREYAVANRFFIYSDALCIMPV 59
    | | : : : | | : : : | | | | | : | | : |
Db 174 VNTLSLIFLFSYIRMLQAIHDSGGMRSTH----SGRENVATFAIYTTDCACLP 229

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Qy 60 FVVKILSLFRVEIPDITMTSMWYIFFLPVNSALNPILYTLTTNFEKDKL 107  
 |||: :| : : : |||||: ||||| : : :  
 Db 230 IVVKIALSGCEISPDLYAMLAVALVLPVNSALNPVLYTLTTAAFRQOL 277

## RESULT 2

Q9VBP0	
ID	Q9VBP0
	PRELIMINARY;
	PRT;
	359 AA

AC Q9VBP0;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT	01-MAY-2000	(TREMBlrel. 13, last sequence update)
DT	01-MAR-2002	(TREMBlrel. 20, last annotation update)

DE CG5042 protein.  
GN CG5042 OR CG5046.

OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachy  
OC Ephydroidea; Drosophilidae; Drosophila.

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OX      NCBI_TaxID=7227;
RN      [1]

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RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
STR-086

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., G

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A.  
RA George R.A., Lewis S.E., Richards S., Ashburner M.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q.,  
RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe N.

RA wan K.H., Doyle C., Baxter E.G., Helt G., Neilsen C.  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I.

RA Borkova D., Botchan M.R., Bouck J., Broksstein P., E  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Cent

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B.,  
de pablos B., Delcher A., Deng Z., Mays A.D., Dew I  
RA

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Du  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera

[illegible]



DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00560; LRR\_14.  
 DR SMART: SM00013; LRRNT; 1.  
 DR PROSITE: PS00339; AA\_TRNA\_LIGASE\_II\_2; UNKNOWN\_1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECP\_FL\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECP\_FL\_2; 1.  
 DR Receptor.  
 KW Receptor.  
 SQ SEQUENCE 1012 AA; 112623 MW; 52A70E7A88CA6E0A CRC64;

Query Match 28.8%; Score 158; DB 5; Length 1012;  
 Best Local Similarity 33.3%; Pred. No. 1.5e-09;  
 Matches 37; Conservative 22; Mismatches 30; Indels 22; Gaps 4;

QY 2 VNLAFLIIFYITMCSIOKTAQTTEVRCNGREVAANRFFVFSDAICWIPV-- 59  
 Db 729 LNLAFVITMACYASIV-----LAIOGSHAMNC--NDSRVARRNSLIVTFDFACWAPIAF 781  
 QY 60 -----FVVKILSLFRVEIPDTMTSMVIFELPVNSALNPILYTLTTFEK 104  
 Db 782 FSULTAFGLRLISLDGAKV-----LTIFVPLNSCANFELYITLTKOK 825

RESULT 4  
 Q95YI7 PRELIMINARY; PRT; 1280 AA.

AC Q95YI7;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Glycoprotein hormone receptor.  
 GN ACPGPH.  
 OS Asterina pectinifera (Starfish).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa; Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.  
 OX NCBI\_TaxID=7594;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mita M., Hirai T., Oba Y., Yoshikuni M., Nagahama Y.;  
 RT "cDNA cloning and functional analysis of a novel member of the glycoprotein hormone receptor family from a starfish Asterina pectinifera."  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB061861; BAB68208.1; -  
 DR InterPro: IPR002106; AATRNA\_LigaseII.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00560; LRR\_14.  
 DR SMART: SM00013; LRRNT; 1.  
 DR PROSITE: PS00339; AA\_TRNA\_LIGASE\_II\_2; UNKNOWN\_1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECP\_FL\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECP\_FL\_2; 1.  
 DR Receptor.  
 KW Receptor.  
 SQ SEQUENCE 1280 AA; 141700 MW; 0A0BEC0CDD880BA CRC64;

Query Match 28.8%; Score 158; DB 5; Length 1280;  
 Best Local Similarity 33.3%; Pred. No. 1.9e-09;  
 Matches 37; Conservative 22; Mismatches 30; Indels 22; Gaps 4;

QY 2 VNLAFLIIFYITMCSIOKTAQTTEVRCNGREVAANRFFVFSDAICWIPV-- 59  
 Db 729 LNLAFVITMACYASIV-----LAIOGSHAMNC--NDSRVARRNSLIVTFDFACWAPIAF 781  
 QY 60 -----FVVKILSLFRVEIPDTMTSMVIFELPVNSALNPILYTLTTFEK 104  
 Db 782 FSULTAFGLRLISLDGAKV-----LTIFVPLNSCANFELYITLTKOK 825

RESULT 5  
 Q8SPS8

ID Q8SPS8 PRELIMINARY; PRT; 701 AA.  
 AC Q8SPS8;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Luteinizing hormone receptor.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HOLSTEIN; TISSUE=CORPUS LUTEUM;  
 RA Kawate N., Tamada H., Inaba T., Sawada T.;  
 RT "Molecular cloning of a full-length cDNA encoding bovine luteinizing hormone receptor and its expression in COS-7 cells."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF491303; AAM09535.1; -  
 DR Receptor.  
 KW Receptor.  
 SQ SEQUENCE 701 AA; 78455 MW; D70AB862EB265CCF CRC64;

Query Match 26.5%; Score 145.5; DB 6; Length 701;  
 Best Local Similarity 29.8%; Pred. No. 2.9e-08;  
 Matches 31; Conservative 24; Mismatches 42; Indels 7; Gaps 2;

QY 2 VNLAFLIIFYITMCSIOKTAQTTEVRCNGREVAANRFFVFSDAICWIPV 61  
 Db 536 LNWAFITICACYIKIFAVQNPFLMAT-----NKDTKAKKAAVLIFDFTCMAPISF 589  
 QY 62 VKILSLFRVE-IPDTMTSMVIFELPVNSALNPILYTLTTFEK 104  
 Db 590 FALSAAKFVPLITVNTSKVLVLFYVPVNSCANFELVAFITKAFQ 633

RESULT 6  
 Q9BN18 PRELIMINARY; PRT; 1050 AA.

AC Q9BN18;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Leucine-rich repeat-containing G protein-coupled receptor 2.  
 GN RK OR CG8930.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Preygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mishi S., Hsu S.Y., Zeli K., Hsueh A.J.;  
 RT "Characterization of two fly LGR (leucine-rich repeat-containing G protein-coupled receptor) proteins homologous to vertebrate RT glycoprotein hormone receptors: constitutively activation of wild type RT fly LGR1 but not LGR2 in transfected mammalian cells."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF274591; AAK00808.1; -  
 DR FlyBase: FBgn0003255; rk.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR003592; LRR\_out.  
 DR InterPro: IPR003591; LRR\_typ.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00560; LRR\_10.  
 DR PRINTS: PR00237; GPCRHHODOPSN.  
 DR SMART: SM00370; LRR; 8.  
 DR SMART: SM00369; LRR\_typ; 10.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECP\_FL\_2; 1.  
 DR Receptor.  
 KW Receptor.  
 SQ SEQUENCE 1050 AA; 117707 MW; 35D71260A8B4BF99 CRC64;

Query Match 25.9%; Score 142; DB 5; Length 1050;

Best Local Similarity 31.4%, Pred. No. 1e-07;  
Matches 33; Conservative 22; Mismatches 40; Indels 10; Gaps 3;

OY 2 VNLAFLIVFESYITMFCISQ-KTALQTEVRNCGREVAANREFEIVFSDAICMIPVF 60  
DB 715 INGCAPFLTMGCYLMKMYAIRGSAQAMNTDSR-----IKRRALLVFTFPLCMSP1A 766

OY 61 VKILSLFVEIPDMTWSI-VIFPLPVNSALNPILYLTITTFK 104  
DB 767 FFSITAFGLQILSLGQAKIFVFLPLNSCNPFLYAITMTQFK 811

RESULT 7  
ID Q9NKM6 PRELIMINARY; PRT; 1300 AA.  
AC Q9NKM6; Q9VJ03;  
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)  
DT 01-OCT-2000 (TREMblrel. 21, last annotation update)  
DE Hypothetical 144.0 kDa protein (Rk gene product).  
GN RK OR CG8930.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RX MEDLINE=99403001; PubMed=10471707;  
RA Ashburner M., Miera S., Roote J., Lewis S.E., Blazej R., Davis T.,  
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,  
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,  
Palazzo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitehead K.,  
Celniker S., Rubin G.M.;  
RT "An exploration of the sequence of a 2.9-Mb region of the genome of  
Drosophila melanogaster: the adh region.";  
RL Genetics 153:179-219(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RX Butenoff C., Champe M., Chavez C., Hew M., Ciesiolka L., Doyle C.M.,  
Farran D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,  
Houston K.A., Hummasti S.R., Karia K., Kearney L., Kim E., Lee B.,  
Lewis S., Li P., Lomont M.A., Mazda P., Moshrefi A.R., Moshrefi M.,  
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,  
Sethi H., Snir E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,  
Zieran L.L., Rubin G.M.;  
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
Abtill J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,  
Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,  
Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
Dodson K., Doup L.E., Downes M., Dugan-Hoch A.S., Dunkov B.C., Dunn P.,  
Dubin K.C., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,  
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
Sper E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
Zhang X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
DR EMBL; AE003408; AAF4846.1; -;  
DR EMBL; AE003642; AAF5367.2; -;  
DR FlyBase; FBgn0032255; rK.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR003592; LRR\_out.  
DR InterPro; IPR003591; LRR\_Typ.  
DR Pfam; PF00001; 7tm1\_1; 1.  
DR Pfam; PF00560; LRR; 10.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR SMART; SM00370; LRR; 1.  
DR SMART; SM00369; LRR\_Typ. 4.  
DR PROSITE; PS50262; G\_PROTEIN\_RECPT\_FL2; 1.  
DR Hypothetical protein.  
SQ SEQUENCE 1300 AA; 144031 MW; B4B9E39F942FA0B3 CRC64;

Query Match 25.9%; Score 142; DB 5; Length 1300;  
Best Local Similarity 31.4%, Pred. No. 1.2e-07;  
Matches 33; Conservative 22; Mismatches 40; Indels 10; Gaps 3;

OY 2 VNLAFLIVFESYITMFCISQ-KTALQTEVRNCGREVAANREFEIVFSDAICMIPVF 60  
DB 869 INGCAPFLTMGCYLMKMYAIRGSAQAMNTDSR-----IKRRALLVFTFPLCMSP1A 920

OY 61 VKILSLFVEIPDMTWSI-VIFPLPVNSALNPILYLTITTFK 104  
DB 921 FFSITAFGLQILSLGQAKIFVFLPLNSCNPFLYAITMTQFK 965

RESULT 8  
ID Q9NDI1 PRELIMINARY; PRT; 1360 AA.  
AC Q9NDI1;  
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)  
DT 01-OCT-2000 (TREMblrel. 20, last annotation update)  
DE Glycoprotein hormone receptor II.  
GN RK OR CG8930.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CANTON S. TISSUE-WHOLE ANIMAL;  
RX MEDLINE=20359836; PubMed=10899142;  
RA Erikson K.K., Hauser F., Schiott M., Pedersen K.-M., Soendergaard L.,  
Grimmelikhuijzen C.J.P.;  
RT "Molecular Cloning, Genomic Organization, Developmental Regulation,  
and a Knock-Out Mutant of a Novel Leu-Rich Repeats-Containing G  
Protein-Coupled Receptor (DLGR-2) from Drosophila melanogaster.";  
RT Genome Res. 10:924-938(2000).  
RL EMBL; AF142343; AAF6608.1; -;

DR HSP: Q57815; 1D3Y.  
 DR Flybase: Fggn0003255; rK.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR003592; LRR\_out.  
 DR InterPro: IPR003591; LRR\_typ.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00560; LRR; 14.  
 DR PRINTS: PR00237; GPCR\_Rhodopsn.  
 DR SMART: SM00370; LRR; 2.  
 DR SMART: SM00369; LRR\_Typ; 5.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEPT\_F1\_2; 1.  
 DR Receptor.  
 SQ SEQUENCE 1360 AA; 150731 MW; 7D435155BAF6F612 CRC64;

Query Match 25.9%; Score 142; DB 5; Length 1360;  
 Best Local Similarity 31.4%; Pred. No. 1.3e-07;  
 Matches 33; Conservative 22; Mismatches 40; Indels 10; Gaps 3;

OY 2 VNLAFLIVFSYITMFCISIQ-KTALQTEVRNCGREAVANRFFETVSDAICMIPVY 60  
 DB 929 INGCALFTLMGCYLNKYNALRGSQAMNTDSR-----IAKRALLVFTDFLCMSPIA 980  
 OY 61 VKILSLFRVEIPDTMTSMI-VIFELPVNSALNPILYTLTTFEK 104  
 DB 981 FFSITAFGLQLISLEQAKIFVFLPLNSCNPFLYALMTKQFK 1025

RESULT 9  
 042500 PRELIMINARY; PRT; 601 AA.

ID 042500;  
 AC 042500;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Luteinizing hormone receptor (fragment).  
 OS Melagris gallinavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Melagrididae; Melagris.  
 OX NCBI\_TaxID=9103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20078926; PubMed=10611074;  
 RX Yau S., Kim H., Hsu C.C., El Halawani M.E., Foster D.N.;  
 RT "Three different turkey luteinizing hormone receptor (LH-R) isoforms  
 RT I: characterization of alternatively spliced LH-R isoforms and their  
 RT regulated expression in diverse tissues.";  
 RL Biol. Reprod. 62:108-116(2000).  
 DR EMBL: U92082; AAB64409.1;  
 DR HSP: P22888; 1LUT.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_Rhodopsn.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEPT\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEPT\_F1\_2; 1.  
 DR Receptor.  
 KW NCBI\_TaxID=9103;  
 FT NON\_TER  
 RN [1]  
 SQ SEQUENCE 601 AA; 67380 MW; 71AD2FD6D5E28FDC CRC64;

Query Match 25.2%; Score 138.5; DB 13; Length 601;  
 Best Local Similarity 28.8%; Pred. No. 1.6e-07;  
 Matches 30; Conservative 23; Mismatches 44; Indels 7; Gaps 2;

OY 2 VNLAFLIVFSYITMFCISIQKTALQTEVRNCGREAVANRFFETVSDAICMIPVY 61  
 DB 432 LNAVAFLVVCACIKIYIVAVNELVAA-----NDTKIAKMAVLIPTDFCMAPISF 485  
 OY 62 VKILSLFRVEIPDTMTSMI-VIFELPVNSALNPILYTLTTFEK 104  
 DB 486 FAISAFKPLITVNSKILLVFPVNSCANPFLAIFTKQ 529

RESULT 10

O9DGC5  
 ID 09DGC5  
 AC 09DGC5; PRELIMINARY; PRT; 693 AA.  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Gonadotropin receptor II.  
 GN TGRH-RII.  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorphia; Acanthopterygii; Perciformes; Perciliformes; Labroidae;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Oba Y., Hirai T., Yoshitani Y., Yao Z., Nagahama Y.;  
 RT "Tilapia gonadotropin receptor II.";  
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.

DR HSP: P22888; 1LUT.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00560; LRR; 2.  
 DR PRINTS: PR00237; GPCR\_Rhodopsn.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEPT\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEPT\_F1\_2; 1.  
 DR Receptor.  
 KW SEQUENCE 693 AA; 77856 MW; C3BBEPD8ECFC0988 CRC64;

Query Match 25.2%; Score 138.5; DB 13; Length 693;  
 Best Local Similarity 28.8%; Pred. No. 1.8e-07;  
 Matches 30; Conservative 23; Mismatches 44; Indels 7; Gaps 2;

OY 2 VNLAFLIVFSYITMFCISIQKTALQTEVRNCGREAVANRFFETVSDAICMIPVY 61  
 DB 534 LNVAVFLVVCYCYICILSVNHESTR-----GDTKIAKMAVLIPTDFCMAPISF 587  
 OY 62 VKILSLFRVEIPDTMTSMI-VIFELPVNSALNPILYTLTTFEK 104  
 DB 588 FAISAFKPLITVNSKILLVFPVNSCANPFLAIFTKQ 631

RESULT 11  
 015996 PRELIMINARY; PRT; 699 AA.  
 ID 015996;  
 AC 015996;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Luteinizing hormone receptor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=OVARY;  
 RX MEDLINE=92017881; PubMed=1922095;  
 RA Jia X.C., Oikawa M., Bo M., Tanaka T., Ny T., Boime I., Hsueh A.J.;  
 RT "Expression of human luteinizing hormone (LH) receptor: interaction  
 RT with LH and chorionic gonadotropin from human but not equine, rat, and  
 RT ovine species.";  
 RL Mol. Endocrinol. 5:759-768(1991).  
 DR EMBL: S57793; AAB19917.2;  
 DR HSP: P22888; 1LUT.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR001611; LRR.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR Pfam: PF00560; LRR; 3.  
 DR SMART: SM00013; LRRNT; 1.



Db 661 FYAMSAVVDRLPITVSNKILIVLEFPPLNSCANPFLYALFTNAFR 705

Search completed: May 22, 2003, 12:47:04

Job time : 86 secs

RX MEDLINE-20462948; PubMed=11006115;  
RA Oba Y., Hirai T., Yoshitura Y., Kobayashi T., Nagahama Y.,  
RT "Cloning, Functional Characterization, and Expression of Thyrotropin  
RT Receptors in the Thyroid of Amago Salmon (*Oncorhynchus rhodurus*).";  
RL Biochem. Biophys. Res. Commun. 276:258-263(2000).  
DR EMBL: AB030954; BAB07800.1; -  
DR HSSP: P16473; 1XDM.  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR InterPro: IPR001611; LRR.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR Pfam: PF00560; LRR; 1.  
DR PRINTS: PR00237; GPCRHHODPSN.  
DR PROSITE: PS00237; G\_GPROTEIN\_RECEPTOR\_FL1; UNKNOWN\_1.  
DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_FL2; 1.  
KW Receptor.  
SQ SEQUENCE 814 AA; 91091 MW; 1FC9A2AEBD6C911E CRC64;

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GenCore version 5.1.4.p5.4578  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 26, 2003, 19:35:57 ; Search time 2362 seconds

(without alignments)  
1318.374 Million cell updates/sec

Title: US-09-930-312-2

Perfect score: 549

Sequence: 1 GVNLLAFLLIVFSYITMFCSS.....NSALNPILYTLTFNFKKXL 107

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: em\_ba : \*  
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17: em\_hum : \*  
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25: em\_pl : \*  
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27: em\_sts : \*  
28: em\_un : \*

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31: em\_htg\_inv : \*  
32: em\_htg\_other : \*  
33: em\_htg\_mus : \*  
34: em\_htg\_pin : \*  
35: em\_htg\_rod : \*  
36: em\_htg\_mam : \*  
37: em\_htg\_vrt : \*  
38: em\_sy : \*  
39: em\_htgo\_hum : \*  
40: em\_htgo\_mus : \*  
41: em\_htgo\_other : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	100.0	321	6 AX384516	AX384516 Sequence
2	549	100.0	1068	6 AX148176	AX148176 Sequence
3	549	100.0	2049	6 AX385037	AX385037 Sequence
4	549	100.0	2142	6 AX451566	AX451566 Sequence
5	549	100.0	2193	6 AX385032	AX385032 Sequence
6	549	100.0	2214	6 AX451562	AX451562 Sequence
7	549	100.0	2265	6 AX385027	AX385027 Sequence
8	549	100.0	2436	9 AF453828	AF453828 Homo sapi
9	549	100.0	2838	9 AF403384	AF403384 Homo sapi
10	478	87.1	2214	6 AX385045	AX385045 Sequence
11	478	87.1	2539	10 AF346501	AF346501 Mus muscu
12	376	68.5	1191	6 AX128507	AX128507 Sequence
13	376	68.5	2274	9 AF190500	AF190500 Homo sapi
14	371	67.6	1018	6 AX147820	AX147820 Sequence
15	371	67.6	170522	9 AL138708	AL138708 Human DNA
16	349	63.6	474	6 AX088165	AX088165 Sequence
17	326.5	59.5	164610	2 AC098990	AC098990 Rattus no
18	326.5	59.5	171869	2 AC121029	AC121029 Rattus no
19	319	58.1	180673	10 AC068627	AC068627 Mus Muscu
20	319	58.1	213462	10 AC077689	AC077689 Mus Muscu
21	255	46.4	187431	9 AC107219	AC107219 Homo sapi
22	253.5	46.2	58377	2 AC128964	AC128964 Rattus no
23	253.5	46.2	124282	2 AC121415	AC121415 Rattus no
24	253.5	46.2	173546	2 AC098607	AC098607 Rattus no
25	251.5	45.8	179055	2 AC122462	AC122462 Mus muscu
26	234	42.6	1015	6 AX254453	AX254453 Sequence
27	225	41.0	1080	6 AX254459	AX254459 Sequence
28	225	41.0	3187	6 AX254458	AX254458 Sequence
29	225	41.0	57274	2 AC017540	AC017540 Drosophi
30	225	41.0	163970	3 AC010580	AC010580 Drosophi
31	225	41.0	167396	3 AC010579	AC010579 Drosophi
32	225	41.0	226332	3 AE003753	AE003753 Drosophi
33	210	38.3	3756	3 LSGPCR	223104 L. steagalis
34	188	34.2	176565	2 AL136106	AL136106 Homo sapi
35	181	33.0	3574	6 AX254452	AX254452 Sequence
36	181	33.0	15570	2 AC014247	AC014247 Drosophi
37	181	33.0	171751	3 AC023697	AC023697 Drosophi
38	181	33.0	174157	3 AC023711	AC023711 Drosophi
39	181	33.0	323461	3 AE003491	AE003491 Drosophi
40	158.5	28.9	137956	2 AC010918	AC010918 Drosophi
41	158	28.8	3942	3 AB061862	AB061862 Aseteria
42	158	28.4	3943	3 AB061861	AB061861 Aseteria
43	156	28.4	171869	2 AC121029	AC121029 Rattus no
44	154	28.1	173546	2 AC098607	AC098607 Rattus no
45	146.5	26.7	5886	10 AF069778	AF069778 Mus muscu

RESULT 1

## ALIGNMENTS

AX384516  
LOCUS AX384516 321 bp DNA linear PAT 19-MAR-2002  
DEFINITION Sequence 1 from Patent WO0214496.  
ACCESSION AX384516  
VERSION AX384516.1 GI:19577719  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS 1  
TITLE Lind, P.  
JOURNAL Novel g protein-coupled receptors  
PATENT: WO 0214496-A 1 21-FEB-2002;  
PHARMACIA & UPJOHN COMPANY (US)  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 76 a 67 c 59 g 119 t  
ORIGIN

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Pred. No.: 2,986-51 Length: 321  
Score: 549.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-930-312-2 (1-107) x AX384516 (1-321)

QY 1 GlyValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer 20  
DB 1 GGTCGAACTTCCTGCTTCCTTCATCATTCGTTTCTTAATTAATGTTCTGTTCC 60  
QY 21 IleGlnLysThrAlaLeuGlnThrGluValArgAsnCysPheGluYrgrGluValAla 40  
DB 61 ATTCAAAAACCGCCCTTCGACACACAGAGTAGGAATGTTTGAGAGAGGTTGCT 120  
QY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60  
DB 121 GTTCGAAATCGTTCTTTTATAGTGTCCTCGATCGCATCGCGATTCCTGTAATT 180  
QY 61 ValValLysIleLeuSerIleuPheArgValGluIleProAspThrMetThrSerTrpIle 80  
DB 181 GTAGTTAAATCCTTCCTTCGCGGAGAAATACACAGACATGACTTCCTGATA 240  
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrTr 100  
DB 241 GTGATTTTTCCTTCCTTCACATTAACAGTCTTGAATCCATTCCTTAATCTCACACC 300  
QY 101 AsnPhePheLysAspLysLeu 107  
DB 301 AACCTTTTAAAGACAGATTG 321

RESULT 2  
AX148176 1068 bp DNA linear PAT 08-JUN-2001  
LOCUS AX148176  
DEFINITION Sequence 17 from Patent WO0136471.  
ACCESSION AX148176  
VERSION AX148176.1 GI:14347081  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS 1 (bases 1 to 1068)  
TITLE Chen, R., Dang, H.T. and Lowitz, K.P.  
JOURNAL Endogenous and non-endogenous versions of human g protein-coupled receptors  
PATENT: WO 0136471-A 17 25-MAY-2001;  
Arena Pharmaceuticals, Inc. (US)

FEATURES  
source Location/Qualifiers  
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ORIGIN

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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-09-930-312-2 (1-107) x AX148176 (1-1068)

QY 1 GlyValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer 20  
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QY 21 IleGlnLysThrAlaLeuGlnThrGluValArgAsnCysPheGluYrgrGluValAla 40  
DB 649 ATTCAAAAACCGCCCTTCGACACACAGAGTAGGAATGTTTGAGAGAGGTTGCT 708  
QY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60  
DB 709 GTTCGAAATCGTTCTTTTATAGTGTCCTCGATCGCATCGCGATTCCTGTAATT 768  
QY 61 ValValLysIleLeuSerIleuPheArgValGluIleProAspThrMetThrSerTrpIle 80  
DB 769 GTAGTTAAATCCTTCCTTCCTTCGCGGAGAAATACACAGACATGACTTCCTGATA 828  
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrTr 100  
DB 829 GTGATTTTTCCTTCCTTCACATTAACAGTCTTGAATCCATTCCTTAATCTCACACC 888  
QY 101 AsnPhePheLysAspLysLeu 107  
DB 889 AACCTTTTAAAGACAGATTG 909

RESULT 3  
AX385037 2049 bp DNA linear PAT 19-MAR-2002  
LOCUS AX385037  
DEFINITION Sequence 11 from Patent WO0214489.  
ACCESSION AX385037  
VERSION AX385037.1 GI:19578160  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS 1  
TITLE Paszty, C.D., Gong, J., Daugherty, B. and Rogers, N.  
JOURNAL Leucine-rich repeat-containing g-protein coupled receptor-8  
PATENT: WO 0214489-A 11 21-FEB-2002;  
Amgen, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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ORIGIN												
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Db	1690	GTTGCAATCGCTTTCTTTTTRATAGTGTCTGTATGCCAATCTGCTGGATTCCTGATTT	1749									
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Db	1870	AACTTTTAAAGACAACTTG	1890									
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DEFINITION	Sequence 5 from Patent WO0226824.											
ACCESSION	AX451566											
VERSION	AX451566.1	GI:21698550										
KEYWORDS	human.											
SOURCE	human.											
ORGANISM	Homo sapiens											
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.											
REFERENCE	1 Feder,J.N., Mintier,G., Ramanathan,C.S. and Hawken,D.R.											
AUTHORS	A novel human g-protein coupled receptor, hgrpm5, expressed											
TITLE	highly in brain and ovarian tissues											
JOURNAL	Patent: WO 0226824-A 5 04-Apr-2002;											
	Bristol-Myers Squibb Company (US)											
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DB:	6	Gaps:	0									

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QY	21	IleGlnIlyStrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAla	40				
DB	1723	ATTCAAAAAACCGCTTCGACACACAGAAAGTAAGCAATTGTTTGAAGAGAGGTGGCT	1782				
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DB	1783	GTITGGAAATCGCTTTCTTTTATAGTGTCTCTGTATGTCATCTGCTGAATTCCTGATTT	1842				
QY	61	ValValIlyIleLeuSerIlePheArgValGluIleProAspThrMetThrSerTrpIle	80				
DB	1843	GAGATTAAATCTTTCTCTCTCCGGGGGAAATACCGACACATGACTTCTCGATA	1902				
QY	81	ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr	100				
DB	1903	GTGATTTTTCCTTCACAGTTAACAGTGGTGTGAATCAATCTCTGATCTGTACAAAC	1962				
QY	101	AsnPhePheIlyAspIlyLeu 107					
DB	1963	AACTTTTAAAGCAAGTTG 1983					
RESULT 5							
LOCUS	AX385032	2193 bp	DNA	linear	PAT 19-MAR-2002		
DEFINITION	Sequence 6 from Patent WO0214489.						
ACCESSION	AX385032						
VERSION	AX385032.1	GI:19578156					
KEYWORDS							
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.						
TITLE	1 Paszty,C.J., Gong,J., Daugherty,B. and Rogers,N.						
JOURNAL	Leucine-rich repeat-containing g-protein coupled receptor-8						
FEATURES	molecules and uses thereof						
SOURCE	Patent: WO 0214489-A 6 21-FEB-2002;						
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	NPITRISQRLFTGNTSLFELSMVNNYLEALPKQWCAQMPOLMWDLGKRRKLYLNTST						
	FLSDSLVLDLSNNTLTLSLPHLFDKLQKLTLSNPLMYLHKRNPSSLKQLOSL						
	DLDEIEIPIANTRMFOPMKLNLSHYEFNPFQCSYAPRHVRLICMPDGLSSPEDLANN						
	ILRFVAVIAITFCGLPVIYGMKSLFAERTTHAMSKIKLCCADCLMGYILPFVGIIF						
	DIKTRGQYOKRALLAMBSVOCRLMGFLAMSTEVSVLLTYLTLEKLVIVFPGVSNR						
	PGKRQTSVILICIMAGFLVAIPEFNKDFGNGVCGNGVCEPLYDQTDIGSKGS						
	LGLEIVNALLAFILIVSYITMFCISIQKTLAQTEVENCGREVAVANREFIIVFSDA						
	ICMPVAVKILSLFREVIEDPTMTSMVIFELFVNSALNPLVLTITLTFPKDKLQQL						
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Alignment Scores:  
Pred. No.: 1.83e-50 Length: 2193  
Score: 549.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-930-312-2 (1-107) x AX385032 (1-2193)  
QY 1 GtYValaAsnLeuLeuAlaPheLeuIleIleValPheSerTyrTlleThrMetPheCysSer 20  
Db 1774 GGTGGAACCTGCTGCTTCTCATCATGTTGTTTCTATATACATGATGTTCTGTTCC 1773  
QY 21 IlegInLysThAlaLeuGInThrThrGluValArgAsnCysPheGlyArgGluValAla 40  
Db 1774 ATTCAAAAACCGCCTTGACACACAGAAAGTAAGGAATGTTTGGAGAGAGCGGCT 1833  
QY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60  
Db 1834 GTTGGAAATCGCTTCTTTTATGTTCTGATGCCATGCTGATGCTGATTT 1893  
QY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetPheSerTrpIle 80  
Db 1894 GTAGTTAAATCTTCCCTTCCTCCGGGTGGAATACCAACACATGACTCTCGATTA 1953  
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100  
Db 1954 GCGATTTTTCCTTCCATTAACAGTGCCTTGAATCCATCTCATATCTCCACAAAC 2013  
QY 101 AsnPhelPheLysAspLysLeu 107  
Db 2014 AACCTTTTAAAGACACAGTTG 2034  
RESULT 6  
LOCUS AX451562 2214 bp DNA linear PAT 03-JUL-2002  
DEFINITION Sequence 1 from Patent WO0226824.  
ACCESSION AX451562  
VERSION AX451562.1 GI:21698547  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Feder, J.N., Muntler, G., Ramanathan, C.S. and Hawken, D.R.  
A novel human g-protein coupled receptor, hgrprbm5, expressed  
highly in brain and ovarian tissues  
Patent: WO 0226824-A 1 04-APR-2002;  
JOURNAL Bristol-Myers Squibb Company (US)  
FEATURES  
source  
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Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 638 a 457 c 416 g 703 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.84e-50 Length: 2214  
Score: 549.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-930-312-2 (1-107) x AX451562 (1-2214)  
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Db 1735 GGTGGAACCTGCTGCTTCTCATCATGTTGTTTCTATATACATGATGTTCTGTTCC 1794  
QY 21 IlegInLysThAlaLeuGInThrThrGluValArgAsnCysPheGlyArgGluValAla 40

|||||  
Db 1795 ATTCAAAAACCGCCTTGACACACAGAAAGTAAGGAATGTTTGGAGAGAGCGGCT 1854  
QY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60  
Db 1855 GTTGGAAATCGCTTCTTTTATGTTCTGATGCCATGCTGATGCTGATTT 1914  
QY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetPheSerTrpIle 80  
Db 1915 GTAGTTAAATCTTCCCTTCCTCCGGGTGGAATACCAACACATGACTCTCGATTA 1974  
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100  
Db 1975 GCGATTTTTCCTTCCATTAACAGTGCCTTGAATCCATCTCATATCTCCACAAAC 2034  
QY 101 AsnPhelPheLysAspLysLeu 107  
Db 2035 AACCTTTTAAAGACACAGTTG 2055  
RESULT 7  
LOCUS AX385027 2265 bp DNA linear PAT 19-MAR-2002  
DEFINITION Sequence 1 from Patent WO0214489.  
ACCESSION AX385027  
VERSION AX385027.1 GI:19578152  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Paszty, C.J., Gong, J., Daugherty, B. and Rogers, N.  
Leucine-rich repeat-containing g-protein coupled receptor-8  
molecules and uses thereof  
Patent: WO 0214489-A 1 21-FEB-2002;  
JOURNAL Amgen, Inc. (US)  
FEATURES  
source  
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Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
1..2265  
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NPITRISORLPTGLNSLEFLSMVNNYIEALPKOKOAKPOLNMDYDEBNRIKYLNTST  
FLSCSLVLPAPRNQIGFVPEKPTSSLNKGEIDLSNTTETLSPLFKDLKLOKL  
NLSSNPMLYLRHNOFESLKOQSLDLERIEIPNITNMFOPKRNLSHYEFNFRCSY  
APHRICMPLIDNGISSFEDLLANNILRIEFVVAITFCGNLFVIGMRSFTKAENTTH  
AMSIRILCCADCLMGVLEFVGIPDKYRGQYKVALAMESVOCRLGFLAMSTEV  
SVLLITVTLLEKELIVTFPPSNIRPKROTSLIILCIMAGFLIAVIPFMKDVGNF  
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EVRNCFGRVAVANRFEIVFSDALCLVFEVVKILSLPVEIPDMTSMVITFFLPV  
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BASE COUNT 650 a 466 c 423 g 726 t  
ORIGIN  
sig\_peptide  
1..108  
Alignment Scores:  
Pred. No.: 1.88e-50 Length: 2265  
Score: 549.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-930-312-2 (1-107) x AX385027 (1-2265)

QY	1	GIYValAsnIleuLeuAlaIlePheIleuIleIleValIlePheSerTyrIleThrMetPheCysSer	20
Db	1786	GGTGGAACTGGCTGGCTTTTCTCATCAATGTGTTTCCATATATACATATGTTCTGTTCC	1845
QY	21	IleGlnIySthrAlaIleGlnIthrThrcIuValAlaIraGncYsPheGIlYArgGluValAla	40
Db	1846	ATTCAAAAAACCGCTTGACAGACCAAGAAAGTAAGTAATGTTTGGAAAGAGGTGGCT	1905
QY	41	ValAlaAsnAargPhePhePheIleValIlePheSerAspAlaIleCysTrpIleProValPhe	60
Db	1906	GTTGCAAAATCCTTTCTTTTATATATGTTCTGTATGCCATCTGCTGGATTCCTATATT	1965
QY	61	ValValIysIleIleSerIleuPheArgValGluIleProAspThrMetThrSerTrpIle	80
Db	1966	GTAGTTAAATTCCTTCCCTCTCCGGGTGGAAATACCAAGACACATATGTTCCGGATA	2025
QY	81	ValIlePhePheIleuProValAsnSerAlaIleuAsnProIleIleuTyrThrIleuThrThr	100
Db	2026	GTGATTTTTCCTTCCTCCAGTTAAACAGTCCTTGATCCAATCCTCATATCTCCACAAC	2085
QY	101	AsnPhePheIySAspIySleu	107
Db	2086	AACITTTTAAAGACAAGCTTG	2106
RESULT 8			
LOCUS	AF453828	2436 bp	mRNA linear PRI 04-FEB-2002
DEFINITION	AF453828	Homo sapiens G protein-coupled receptor affecting testicular	
VERSION	AF453828	descent (GREAT) mRNA, complete cds.	
KEYWORDS	AF453828.1	GI:18483167	
SOURCE		Homo sapiens.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	
AUTHORS		Mammalia: Eutheria: Primates; Catarrhini; Homnidae; Homo.	
TITLE		1 (bases 1 to 2436)	
JOURNAL		Gorlov,I.P., Kanat,A., Jones,E., Lamb,D., Truong,A., Bogatcheva,N.,	
REFERENCE		Bishop,C.E., McCreavey,K. and Agoulnik,A.I.	
AUTHORS		Mutations of the GREAT gene cause cryptorchidism	
TITLE		2 (bases 1 to 2436)	
JOURNAL		Agoulnik,A.I.	
REFERENCE		Direct Submission	
AUTHORS		Submitted (30-NOV-2001) Ob/Gyn, Baylor College of Medicine, 6550	
TITLE		Fannin St., Su. 861, Houston, TX 77030, USA	
JOURNAL		Location/Qualifiers	
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		descent"	
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		NTLRKIFIEHLNHCIRHISRKAFEGICNQLIYLNHNCITTLRPGLFKDHLTWLIDDD	
		TKTIRISQRLFTGINSIFLPSWANNLEALPKQWCAQMPQUNWVDEGNRIKYLTNST	
		FLSDSLTVLFLPNOIGVPERKFSISKINIGELDISSNTITELSPHFDKLLQKLL	
		NLSNPLMYLHKNOFESIKOLOSLDERIEIPNTNTPMQPMKLSHIFKRNPKCYG	
		APHRICTMPLELTIGSSPEDILANNILIFIPWVAFITCPGNLPIFGMSRIRKANTHY	
		AMSKITLCCADCLMGVLFYFGVIFDIKRYQKYALIMHMSVQCRMLGLANLSTEV	
		SVLLTITLLEKELVIVFSPNSIRPGRKQTSVLLICIMWAGFLVAPFNKKDIFGNF	
		YKNGKGVFLPYDQTEDIGSKYSGLGIFGLVNLALFLIVFSYITMFCSSLOKALQTT	
		EVKRCFEREVAVANREFEIVFESADICWIPAVVAKIISLFEVEIIPDTMTSMIVIFLTPV	

BASE COUNT	703 a	503 c	456 g	774 t
ORIGIN	NSA/NP/LP/LIT/TN/FE/KDK/LK/LH/KH/KRS/IF/KIK/KS/UST/ST/IW/IED/SS/LK/LGV NKT/LT/GS/IM/KPS"			
Alignment Scores:				
Pred. No.:	2.02e-50	Length:	2436	
Score:	549.00	Matches:	107	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	9	Gaps:	0	
US-09-930-312-2 (1-107) x AF453828 (1-2436)				
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Db 1856	GGTGTGAACCTTGCTGCTTTTCTCTCATCTGTTCTGTTCTCTATATCTATCTGTCTCC 1915			
QY 21	IleGlnIysThrPalaLeuGlnThrGluValArgAsnCysPheGlyArgGluValAla 40			
Db 1916	ATTCAAAAACCGCCTTCAGACACACAGAAGAAAGAAATGTTTGGAAAGAGAGGTGGCT 1975			
QY 41	ValAlaAsnArcPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60			
Db 1976	GTTGCAATTCGTTCTTTTATAGTGTTCCTGTATGCATCTGCTGGATTCCTGTATT 2035			
QY 61	ValValIysIleLeuSerLeuPheArgValGluIleProAspThrMetThrSerTrpIle 80			
Db 2036	GTAGTTAAATCCCTTCCCTTCCTCCGGGTGGAATACACAGACACAAATGACTTCCGATA 2095			
QY 81	ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100			
Db 2096	GTGATTTTTCCTTCCTCCAGTTAACAGTCTTGATTCATTCATCTTATCTCTACCAAC 2155			
QY 101	AsnPhePheIysAspPlysLeu 107			
Db 2156	AACTTTTAAAGAGCAAGTTG 2176			
RESULT 9				
AF403384				
LOCUS				
DEFINITION	Homo sapiens LGR8 mRNA, complete cds.			
ACCESSION	AF403384			
VERSION	AF403384.2 GI:18702459			
KEYWORDS				
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 2838)			
JOURNAL	Hsu,S.Y., Nakabayashi,K., Nishi,S., Kumagai,J., Kudo,M.,			
MEDLINE	Sherwood,O.D. and Hsueh,A.J.			
PUBMED	Activation of orphan receptors by the hormone relaxin			
REFERENCE	Science 295 (5555), 671-674 (2002)			
AUTHORS	2 (bases 1 to 2838)			
TITLE	Hsu,S.Y., Nakabayashi,K. and Bhalla,A.			
JOURNAL	Direct Submission			
REFERENCE	Submitted (26-JUL-2001) GYN/OB, Stanford University, MSOB 5385,			
AUTHORS	Stanford, CA 94305, USA			
TITLE	3 (bases 1 to 2838)			
JOURNAL	Hsueh,A.J.W.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (19-FEB-2002) Division of Reproductive Biology,			
TITLE	Department of Gynecology and Obstetrics, Stanford University			
JOURNAL	Medical Center, 300 Pasteur Drive, Room A-344, Stanford, CA			
REFERENCE	94305-5317, USA			
AUTHORS	Sequence update by submitter			
TITLE	On Feb 19, 2002 this sequence version replaced gi:18419431.			
JOURNAL	Location/Qualifiers			
REMARK	1..2838			
FEATURES				
COMMENT				
source				

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TKLKKIFQHCIRHISKRAFFGLCNLDILVNHNCITTLTRGIFKDLHQLWMLDD
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FLSCDSLVLFLPRNOIGFVEPKTFSSLNKGEIDLSNTITTELSPLFKDLQKL
NLSSNPFLYLRHNOFESLQSLDLERIEIPNITRMFOPMKNSHLYFKNFRCSY
APHYRICKPLDGISSFEDLLANNIRIEFWAVIAITCGNLFWIGMSFKAEETH
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SVLLITITLEKFLYIVYFPFSNIRGRQTSVILICTMAGFLIATVPMNKDYFNG
YKNGVCPPLYVDIEDIGSGYSLGIFLVGNLAEFLIVSYITMFSIQYALQIT
EVKRCFGREVAVANRPFPIVPSDAICWIPVEVKILSLFVEIPDTMSVIVPELPY
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BASE COUNT 817 a 616 c 536 g 869 t  
ORIGIN

## Alignment Scores:

Pred. No.: 2,33e-50 Length: 2838  
Score: 549.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-930-312-2 (1-107) x AF403384 (1-2838)

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Oy 21 IleglnLysThrAlaLeuGlnInThrThrgluValArgAsnCysPheGlyArggluValAla 40
|||||
Db 1952 ATTCAAAAACCGCCTTGAGACACACAGACAGTAAAGTATGTTTGGAAAGAGGGGCT 2011
Oy 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValAlpe 60
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Db 2012 GTTGCAATTCGTTCTTTTATGTTCTGATGTCATCGCATCGGATGATCTCTGATATT 2071
Oy 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrmethSerTrpIle 80
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Db 2072 GTAGTAAACCTGTTCCCTTCGCGGAGAAATACCGACACAAATGACTTCCTGGATA 2131
Oy 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrlThrLeuThrThr 100
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Db 2132 GGATTTTTCCTTCCAGTAAAGTGTGTTGAATCCATCTCTATATCTCTCACAAAC 2191
Oy 101 AsnPhelPheLysAspLysLeu 107
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Db 2192 AACTTTTAAAGACAAAGTTG 2212
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## RESULT 10

LOCUS AX385045 2214 bp DNA linear PAT 19-MAR-2002  
DEFINITION Sequence 19 from Patent WO0214489.  
ACCESSION AX385045  
VERSION AX385045.1 GI:19578166

## KEYWORDS

## SOURCE

house mouse.  
Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Paszty,C.J., Gong,J., Daugherty,B. and Rogers,N.  
AUTHORS

TITLE Leucine-rich repeat-containing g-protein coupled receptor-8  
JOURNAL molecules and uses thereof  
Patent: WO 0214489-A 19 21 -FEB-2002;  
Amgen, Inc. (US)

## FEATURES

source Location/Qualifiers  
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## CDS

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BRAEFGKDLNLIIVYSHNCITSLRGITRKDLHQLWMLDDNPTRISQRLFTGL
EFLSMVNRRLGKQYKALIMESVOCRLMGPLAMSTEYSVLLITITLEKFLYIV
GVEPKTSSLNKGEIDLSNMITKLFVHLESDHLQKLNLSNPILYVHKRNGFS
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EDLANSGLIRSVWVIAITCGNPLVAVRSLIKAEETHAMSLIKLCCADCLMGVY
LESVGFPIKRYGQYKALIMESVOCRLGFLATLSTEVSLKFLTEKFLYIV
FPESNLRLGKQYKALIMESVOCRLGFLATLSTEVSLKFLTEKFLYIV
FGSRGYSIGITGLVNLAVIYVIVSYVMFCSIKHTALOTAEVRSHIGREYVANRPF
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BASE COUNT 554 a 548 c 492 g 620 t  
ORIGIN

## sig-peptide

554 a 548 c 492 g 620 t

## Alignment Scores:

Pred. No.: 9.93e-43 Length: 2214  
Score: 478.00 Matches: 92  
Percent Similarity: 93.46% Conservative: 8  
Best Local Similarity: 85.98% Mismatches: 7  
Query Match: 87.07% Indels: 0  
DB: 6 Gaps: 0

US-09-930-312-2 (1-107) x AX385045 (1-2214)

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Oy 1 G1yValaAsnLeuLeuAlaPheLeuIleIleValPheSerTyrlIleThrmethCysSer 20
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Db 1735 GGTGGAACCTGCTGGCTTTCTCATCATGTTGTTTCTTAATTAATCATGTTCTGTTCC 1794
Oy 21 IleglnLysThrAlaLeuGlnInThrThrgluValArgAsnCysPheGlyArggluValAla 40
|||||
Db 1795 ATTCATTAACACCGCCTTGACACTGCAGAAAGTACGACATCGGAAAGAGGGGCT 1854
Oy 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValAlpe 60
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Db 1855 GTTGCAACCGGCTTTTATGCGTTCTGATGTCATCGCATCGGATGATCTCTGATATT 1914
Oy 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrmethSerTrpIle 80
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Db 1915 GTGCTTAATATCTGCTCTCTCAAGTGAAGATACCGACACATCACTCTCTGATAC 1974
Oy 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrlThrLeuThrThr 100
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Db 1975 GTGCTTTTTCCTTCCGCGGAGAAACCCATTAACCCATCTCTACACTCTGACAGAC 2034
Oy 101 AsnPhelPheLysAspLysLeu 107
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Db 2035 TCCTTTTAAAGACAAAGTTG 2055
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## RESULT 11

LOCUS AF346501 2539 bp mRNA linear ROD 01-OCT-2001  
DEFINITION Mus musculus G protein coupled receptor affecting testicular  
descent (Great) mRNA, complete cds.  
ACCESSION AF346501  
VERSION AF346501.1 GI:15811372

## KEYWORDS

Mus musculus.

ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS	1 (bases 1 to 2539)
TITLE	Overbeek,P.A., Gorlov,I.P., Sutherland,R.W., Houston,J.B., Harrison,W.R., Boettger-Tong,H.L., Bishop,C.E. and Agoulnik,A.I. A transgenic insertion causing cryptorchidism in mice
JOURNAL	Genesis 30 (1), 26-35 (2001)
MEDLINE	21250990
PUBMED	11353515
REFERENCE	2 (bases 1 to 2539)
AUTHORS	Agoulnik,A.I.
TITLE	Direct Submission
JOURNAL	Submitted (06-FEB-2001) DB/Gyn, Baylor College of Medicine, 6550 Fannin Str. Su. 861, Houston, TX 77030, USA
FEATURES	Location/Qualifiers
source	1..2539
gene	/organism="Mus musculus" /strain="C57BL/6" /db_xref="taxon:10090" /chromosome="5" 1..2539 /gene="Great" 194..2407 /gene="Great" /note="Great" /codon_start=1 /product="G protein coupled receptor affecting testicular descent" /protein_id="A108943.1" /db_xref="GI:15811373" /translation="MMLLVHLLTEVKDFALADSSWVPLCPKGPFGCNCPLRPAHFDVDCDNGNGADENCGDTSGWTFIFGVHGNVKKVLTLCGFCISYQPHQCYEE NELEPCVKADIKAPKVSNNYTLISLKKRHLRPKYSFTELRKIYLDNCNTHIS RRAFLGHNLIQILYLSHNCITLSPGCIKDLQHLAMLLDNPTRISQSFQNSL FFLPMVGNRLALPETLCAQMPQLMWVDLANNIKYITNSTPLTDSLVLPRLNIG GVPDEKSFSSKLNIGEDLSSNMPTKLPHVLFSDHLQKLNLSNPLLVKNOFGSS LKQLOSDLERIEIPNISTGMPQMKMLSHIYLETFRYCSVPVHRIKCMSTGSISS EDLLANGILIRSVWVIAFTICGVGLIVAIRSLIKAEINTHAMSIRILCCADCLMGVY LFSVGDIKIRYGGQYKVALLMMSVSCRIPLGFLATSTEVSYLLFELTLEKTVIV PPSNRIELKRRQPAVALASITWYGFLLAAPPTREDYEGNFGYNGNCFPLHDDAD FGSBYSGLGIFGLVNLALFALIVATISYTWGTSIHKTLQTAENVSHIIGLEAAVNRFF FTVFSDAICWIPVFNKILSLLOVEIPGTTSMWIVFELPVNSALNPLILVLTTSFPR DKLQKLLHKRRKRIFPKVKKSSLASIIVMTDESLKGLVSLALGDSIMKPVSP"
CDS	
BASE COUNT	639 a 641 c 574 g 685 t
ORIGIN	
Alignment Scores:	
Pred. NO.:	1.13e-42
Score:	478.00
Percent Similarity:	93.46%
Best local Similarity:	85.98%
Query Match:	87.07%
DB:	Indels: 0 Gaps: 0
US-09-930-312-2 (1-107) x AF346501 (1-2539)	
OY	1 GIVVAlaAsnLeuLeuAlaPheLeuLeuLeuAlaPheSerTyrlleThrMetPheCysSer 20
Db	1928 GGTGGAACTGCTGGCTTTCCTCGTCATCGGATGATTCCTATAGTCACATCGTTCGCCGC 1987
OY	21 IleglnLvsThrAlaLeuGlntHrThrCrluValuAlaArgAsnCysPheglYArgGluValAla 40
Db	1988 ATTCAATAAACAGCCCTTCAGACTGCACAAAGTGAAGACCAACATCGGAGAGAGGTGCT 2047
OY	41 ValAlaAsnArgPhePhePheLeuAlaPheSerAspAlaIleCysTrpIleProValPhe 60
Db	2048 GTTGCAGAACCGGCTCTTTTATCTGTCCTCTGATGACCATCTGCTGCATCCCTGTGTT 2107
OY	61 ValValLvsIleLeuSerLeuPheArgValAlaGluIleProAspThrMetThrSerTrpIle 80
Db	2108 GTCGTTAAGATCTCTGCTCTTCAAGTGGAGATACACAGGCACATACATCTCGTGGATC 2167

QY	81	ValIIEpHePheLeuProValaIsnSerhAlaIsnPrColleLeuTyThrLeuThrThr	100
Db	2168	GGGGTTTTTTTCCCTCCGGTGAACAGCGCCTTAAACCCCATCTCTACACCTTGACGACC	2227
QY	101	AsnPhenelyAspLySLeu	107
Db	2228	TCCCTTTTAAAGCAAGCTG	2248
RESULT 12			
LOCUS	AX128507	1191 bp	DNA
DEFINITION	Sequence 15 from Patent WO0131014.		Linear
ACCESSION	AX128507		
VERSION	AX128507.1	GI:14134974	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 1191)		
TITLE	Vogeli,G., Wood,L.S. and Merchant,K.		
JOURNAL	G protein-coupled receptors expressed in brain		
	Patent: WO 0131014-A 15 03-MAY-2001;		
	PHARMACIA & UPJOHN COMPANY (US)		
FEATURES	Location/Qualifiers		
Source	1..1191		
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CDS	/db_xref="taxon:9606"		
	1..1191		
	/note="unnamed protein product"		
	/codon_start=1		
	/protein_id="CAC38938.1"		
	/db_xref="GI:14134975"		
	/translation="MFRPLVLSHYPERKFEQYCGYAPRHVSCKPMDGISLLENLLAS		
	IIORFVWVSAVFCGNIFVYICMRPYIRENKLYAMSIISLCCADCLMGIVLEFVIGG		
	FDLKRGEYNNHQAOLMSESHFHCOLVSLITLSEVSLTLPLTLLEKIVIVPEPCV		
	RPGRCRTIVYLILWITGRTIYAFIPLESKPEFRKYVYTNVCYPLHSDPESIGAOIT		
	SVAFLEGLNLAFLIVYISTGSMSTVSHQSYITREIRNWKEMILLAKREFVIFD		
	ALACIPLEFVKELSLQVEIPGTTTSWVFILPINSALPILYTLTRPDKMIRF		
	WYNRRKSRMSDKQKTYAPSFIVEMWMPLOEMPELMKPDLETTYPCEMSLISOSTRL		
	NSYS"		
BASE COUNT	340 a 229 c 226 g 396 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	7.09e-32	Length:	1191
Score:	376.00	Matches:	69
Percent Similarity:	83.18%	Mismatch:	20
Best Local Similarity:	64.49%	Indels:	0
Query Match:	68.49%	Gaps:	0
DB:			
US-09-930-312-2 (1-107) x AX128507 (1-1191)			
QY	1	GIYValAsnLeuLeuAlaPheLeuIleIleValaPheSerTYrIleThrMetPheCysSer	20
Db	673	GGTATTATTATGGCGCGCATTTATCATCATAGTTTTCCTATGGAGCATGTTTATAGT	732
QY	21	IIEGInLySThAlaIeUcLInThrhcGluValaAganCysPheGlyArgGluValaAla	40
Db	733	GGTCATCAAAAGGCGCATTAACAGCACTGAATAATACGGAATCAAGTTAAAAAGAGATGATC	792
QY	41	ValAlaAsnArgPhePhePheIleValaPheSerAspAlaIleCysTrpIleProValaPhe	60
Db	793	CTTGCAAAACGTTTTTCTTATAGTATTACTGATGTCATTAAGTGATACCATTTT	852
QY	61	ValValIlySLIeUeSerLeuPheArgValaGluIleProAsPThrMetThrSerTriple	80
Db	853	GTAAGTAATTTCTTTCCTACTGCTCAGGTAGTAATAACAGGATACCATTAACCTCTGGGTA	912
QY	81	ValIIEpHePheLeuProValaIsnSerhAlaIsnPrColleLeuTyThrLeuThrThr	100
Db	913	GGGATTTTTATCTCCCATTAACAGTCTTTGAACCCCAATTCCTATAACCTTGACGACA	972

[illegible]

Db	1756	GGTATTAAATTTGGCCGCAATTATCATCATAGTTTTTTTCCATAGGAAGCATGTTTATAGT	1815
Oy	21	lleglnlvsfthralaleuglnlthtrhgluvalaragascnysphecglyarggluvalala	40
Db	1816	GTTCATCAAGGCGCATTAACAGCAACTGAAATACCGAATCAAGTTMAAAAGAGATGATC	1875-
Oy	41	ValAlaasnaacgphPhePhePheValaPheSerAspAlaIleCysTrpIleProValPhe	60
Db	1876	CTTGCCAAACGTTTTTTCTTTATAGTATTACTGATGCATTAAGTGGATACCACTTTTTT	1935
Oy	61	ValValylsIleLeuSerIleuPheArgValGluIleProAspThrMetThrSerTrpIle	80
Db	1936	GTAGGAATTTCTTTCACTGCTTAGAGTAGAAATACAGGATACATCAACCTTGGGTA	1995
Oy	81	ValIlePhePheIleProValAsnSerAlaIleuAsnProIleLeuTrpThrIleuThrThr	100
Db	1996	GTGATTTTATTCTGCCCATTACAGTGCCTTGAACCCAAATTCCTATACCTGACACAA	2055
Oy	101	AsnPhePheLysAspLysIleu	107
Db	2056	AGACCATTTAAAGAAATGATTT	2076
RESULT 14			
LOCUS	AX147820/c	1018 bp	DNA linear PAT 08-JUN-2001
DEFINITION	Sequence 65 from Patent WO0136473.		
ACCESSION	AX147820		
VERSION	AX147820.1	GI:14346831	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Enxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1018) Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P., Slightom,J., Schellin,K.A., Kayes,P.S., Bannigan,C.M., Ruff,V., Sejltz,T. and Huff,R.M. Novel q protein-coupled receptors Patent: WO 0136473-A 65 25-MAY-2001; PHARMACIA & UPJOHN COMPANY (US)		
TITLE	Novel q protein-coupled receptors		
JOURNAL	PHARMACIA & UPJOHN COMPANY (US)		
FEATURES	Location/Qualifiers		
source	1..1018		
BASE COUNT	332 a 179 c 189 g 318 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	2,14e-31	Length:	1018
Score:	371.00	Matches:	73
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	67.58%	Indels:	0
DB:	6	Gaps:	0
US-09-930-312-2 (1-107) x AX147820 (1-1018)			
Oy	1	GIYValaasnleuLeuAlaIleuAlaPheleuIleIleValaPheSerTyrlleThrMetPheCysSer	20
Db	539	GGTGGAACCTGTCGTCGCTTTCTCATCATGTTGTTTCCATATATACATATGTTCTGTTCC	480
Oy	21	lleglnlvsfthralaleuglnlthtrhrgluvalaragascnysphecglyarggluvalala	40
Db	479	ATTCAAAAACCGCTTCTGACAGCCACAGAAAGATGATTTGTTGGAAGAGAGTGGCT	420
Oy	41	ValAlaasnaargPhePhePheIleValaPheSerAspAlaIleCysTrpIleProValPhe	60
Db	419	GTTGCAAAATCGTTCTTTTATAGTGTCTCTGATGCATCTGCTGGATTCCTGATTT	360
Oy	61	ValValylsIleLeuSerIleuPheArgValGluIlePro	73
Db	359	GTAGTTAAATCTCTTCCCTTCGCGGATGGAATACCA	321

RESULT 15  
AL138708 170522 bp DNA linear PRI 01-FEB-2001  
LOCUS Human DNA sequence from clone RP11-432E15 on chromosome 13 contains  
DEFINITION STS, GSSs and a Cpg island, complete sequence.  
ACCESSION AL138708  
VERSION AL138708.17 GI:11137618  
KEYWORDS HTG; Cpg Island.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 170522)  
AUTHORS Philimore, B.  
TITLE Direct Submission  
JOURNAL Submitted (01-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquyer@sanger.ac.uk  
requests: clonerequests@sanger.ac.uk  
On Nov 10, 2000 this sequence version replaced gi:11121365.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em; EMBL; SW; SWISSPROT; Tr; TrEMBL; Wp; WORMPEP; Information  
on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 13, constructed by the Sanger Centre Chromosome 13  
Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr13  
This sequence is the entire insert of clone RP11-432E15. The true  
left end of clone RP11-154I23 is at 137612 in this sequence. The  
true right end of clone RP11-95M14 is at 13246 in this sequence.  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated repeat sequence elements. Where the sequence is  
ambiguous, there is an annotation using the 'unsure' feature key.  
RP11-432E15 is from the library RPCI-11.2 constructed by the group  
of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBACE3.6.

FEATURES  
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Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="13"  
/clone="RP11-432E15"  
/clone\_lib="RPCI-11.2"  
19..289  
misc\_feature  
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194..299  
repeat\_region  
/note="53 copies 2 mer tg 71% conserved"  
208..299  
repeat\_region  
/note="23 copies 4 mer tg 77% conserved"  
1456..1750  
repeat\_region  
/note="AluX repeat: matches 3..300 of consensus"  
2078..2183  
repeat\_region  
/note="MIR repeat: matches 6..114 of consensus"  
2600..3122  
misc\_feature  
/note="match: GSS: Em:AQ529216"  
2646..2940  
repeat\_region  
/note="AluSg repeat: matches 1..302 of consensus"  
3590..3894  
repeat\_region  
/note="AluSq repeat: matches 1..296 of consensus"  
3926..4462  
repeat\_region  
/note="L2 repeat: matches 2233..2750 of consensus"  
4658..4805  
repeat\_region  
/note="L2 repeat: matches 2355..2503 of consensus"

repeat\_region  
4911..5224  
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5237..5332  
repeat\_region  
/note="L2 repeat: matches 2575..2694 of consensus"  
5788..6085  
repeat\_region  
/note="AluDo repeat: matches 3..301 of consensus"  
7355..7747  
misc\_feature  
/note="sequence from overlapping clone BA15909  
(AL136106). Assembly confirmed by restriction digest."  
7388..7487  
repeat\_region  
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7396..7487  
repeat\_region  
/note="23 copies 4 mer at 66% conserved"  
7884..7915  
repeat\_region  
/note="MER20 repeat: matches 30..62 of consensus"  
7916..8219  
repeat\_region  
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8220..8376  
misc\_feature  
/note="MER20 repeat: matches 62..210 of consensus"  
8975..8985  
/note="sequence from overlapping clone  
BA15909(AL136106). Assembly confirmed by restriction  
digest."  
9078..9121  
repeat\_region  
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complement(9603..10104)  
misc\_feature  
/note="match: GSS: Em:AQ569313"  
11234..11331  
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(AL136106). Assembly confirmed by restriction digest."  
complement(11953..12400)  
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12477..12601  
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12713..12980  
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(AL136106). Assembly confirmed by restriction digest."  
13272..13417  
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misc\_feature  
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misc\_feature  
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(AL136106). Assembly confirmed by restriction digest."  
13864..14087  
repeat\_region  
/note="L2 repeat: matches 2515..2750 of consensus"  
16061..16342  
repeat\_region  
/note="MER1B repeat: matches 1..244 of consensus"  
16343..16655  
repeat\_region  
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16656..16680  
repeat\_region  
/note="MER1B repeat: matches 244..305 of consensus"  
complement(17019..17275)  
misc\_feature  
/note="match: GSS: Em:AQ452676"  
17070..17578  
/note="match: GSS: Em:AQ511484"  
17087..17515  
misc\_feature  
/note="match: GSS: Em:AQ817416"  
17278..17794  
repeat\_region  
/note="match: GSS: Em:AQ358157"  
18301..18381  
misc\_feature  
/note="L1MB2 repeat: matches 6082..6166 of consensus"  
complement(18563..19010)  
repeat\_region  
/note="match: GSS: Em:AQ242897"  
20403..20559  
repeat\_region  
/note="MER20 repeat: matches 1..153 of consensus"  
20870..21069  
repeat\_region  
/note="100 copies 2 mer tt 69% conserved"  
20937..21076  
repeat\_region  
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21080..21392





GeneCore version 5.1.4.p5.4578  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 26, 2003, 19:02:42 : Search time 236 Seconds

(without alignments)  
1021.033 Million cell updates/sec

Title: US-09-930-312-2

Perfect score: 549  
Sequence: 1 GVNLLAFLIVFSYIMFCS.....NSALNPLVLTITNFKDXL 107

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cd1  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MTLEN=0 -MAXLEN=200000000  
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-NO\_XLPHY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -MAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	100.0	321	24 AAD32027	Human novel G-prot
2	549	100.0	1065	24 ABL40194	Human G protein-co
3	549	100.0	1068	22 AAS07943	Human CDNA encodin
4	549	100.0	1473	24 ABL40192	Human G protein-co
5	549	100.0	1545	24 ABL40191	Human G protein-co
6	549	100.0	1830	24 ABL40188	Human G protein-co
7	549	100.0	2142	24 ABR51947	CDNA encoding huma
8	549	100.0	2190	24 ABL40197	Human G protein-co
9	549	100.0	2214	24 ABR51944	CDNA encoding huma
10	549	100.0	2262	24 ABL40196	Human G protein-co
11	376	68.5	530	22 AA199584	Human expressed po
12	376	68.5	530	22 AAL35644	Human musculoskele
13	376	68.5	530	22 ABA06471	Human CDNA SEQ ID
14	376	68.5	530	22 AAS28950	CDNA encoding for
15	376	68.5	530	22 AAS29573	Human endocrine po
16	376	68.5	530	22 AAS30187	DNA encoding rena
17	376	68.5	530	22 AAS34845	DNA encoding nove
18	376	68.5	530	22 ABR43875	DNA encoding novel
19	376	68.5	1089	22 AA199557	DNA expressed po
20	376	68.5	1162	23 ABR43573	DNA encoding novel
21	376	68.5	1191	22 AAD06507	Human GPCR protein
22	376	68.5	1804	21 AA290524	Human GPCR protein
23	376	68.5	2467	20 AA225345	Human LGRT long fo
24	376	68.5	3584	20 AA225346	Human GPCR57 codi
25	371	67.6	1018	21 AAH51001	Human ORFX ORF1290
26	370	67.4	420	21 AAC75735	Human HGR101 G-pr
27	349	63.6	474	22 AAR28059	CDNA encoding Dros
28	234	42.6	1015	22 AAS57085	Drosophila melanog
29	234	42.6	1015	23 ABL07293	CDNA encoding Dros
30	225	41.0	1080	22 AAS57089	Drosophila melanog
31	225	41.0	1080	23 ABL08799	DNA encoding Dros
32	225	41.0	3187	22 AAS57088	DNA encoding Dros
33	225	41.0	3187	23 ABL08798	Drosophila melanog
34	225	41.0	3494	23 ABL08218	Drosophila melanog
35	181	33.0	3574	22 AAS57084	DNA encoding Dros
36	181	33.0	3574	23 ABL07292	Drosophila melanog
37	158.5	28.9	3578	23 ABL03716	Drosophila melanog
38	142.5	26.0	2115	22 ABL01120	Exon 4 of Human lu
39	142	25.9	2586	22 AAH49414	D. melanogaster pe
40	142	25.9	3909	23 ABL14533	Drosophila melanog
41	142	25.9	12248	23 ABL14532	Drosophila melanog
42	138.5	25.2	1831	16 AAQ97312	Rat A3 adenosine r
43	136.5	24.9	2902	11 AAQ06633	Clone encoding rat
44	135.5	24.7	2987	13 AAQ22937	Sequence encoding
45	128	23.3	1681	22 AAH17465	Human CDNA sequenc

## ALIGNMENTS

RESULT 1	
AAD32027	
ID AAD32027 standard; DNA; 321 BP.	
XX	
AC AAD32027:	
XX	
DT 18-JUN-2002 (first entry)	
XX	
DE Human novel G-protein coupled receptor (ncPCR)-1079 DNA.	
XX	
KW Human; novel G-protein coupled receptor; ncPCR-1079; viral infection;	
KW gene; therapy: human immunodeficiency virus; HIV; pain; migraine;	
KW central nervous system disorder; stroke; manic depression; obesity;	
KW metabolic disorder; anorexia; cardiovascular disorder; type 2 diabetes;	
KW cancer; myocardial infarction; hypotension; degenerative disorder;	
KW Parkinson's disease; Alzheimer's disease; neurological disorder;	
KW schizophrenia; anxiety; inflammatory condition; rheumatoid arthritis;	
KW thyroid disorder; autoimmune disorder; hormonal disorder; renal failure;	

KM psoriasis; movement disorder; analgesic; cytostatic; neuroprotective;  
 KM anorectic; hypotensive; hypertensive; tranquilizer; anticonvulsant;  
 KM metabolic; neuroleptic; thrombolytic; cardiant; immunosuppressive; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..321  
 FT /tag= a  
 FT /product= "Human ngPCR-1079 protein"  
 FT /note= "CDS does not include start and stop codon"  
 FT /partial  
 PN WO200214496-A2.  
 PD 21-FEB-2002.  
 XX 15-AUG-2001; 2001WO-US25513.  
 PF 15-AUG-2000; 2000US-225262P.  
 XX  
 PR (PHAA ) PHARMACIA & UPJOHN CO.  
 PA  
 XX Lind P;  
 PI  
 XX WPI: 2002-269192/31.  
 DR P-PSDB: AAE20148.  
 XX  
 XX An isolated nucleic acid molecule encoding novel G-protein coupled  
 PT receptor polypeptide which is useful for treating obesity, diabetes,  
 PT Parkinson's disease, manic depression, migraine, rheumatoid arthritis  
 PT  
 XX  
 PS Claim 4; Page 60; 93pp; English.  
 XX  
 CC The patent discloses novel G-protein coupled receptor (ngPCR)-1079 genes  
 CC and their corresponding proteins. Sequences of the invention are useful  
 CC for treating diseases such as viral infections caused by human immuno-  
 CC deficiency virus (HIV)-1 or 2, central nervous system (CNS) disorders  
 CC (e.g. pain, including migraine, stroke, manic depression), metabolic  
 CC disorders (e.g. obesity and anorexia), cancers, cardiovascular disorders  
 CC (e.g. type 2 diabetes, myocardial infarction, hypertension), degenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease), neurological  
 CC disorders (e.g. schizophrenia and anxiety), inflammatory conditions,  
 CC rheumatoid arthritis, thyroid disorders, autoimmune disorders, hormonal  
 CC disorders, renal failure, psoriasis and movement disorders. The present  
 CC sequence is a DNA encoding human ngPCR-1079 protein.  
 XX  
 SQ Sequence 321 BP; 76 A; 67 C; 59 G; 119 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3.11e-58 Length: 321  
 Score: 549.00 Matches: 107  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-930-312-2 (1-107) x AAD32027 (1-321)  
 QY 1 GYVALASNLLEUVALAPHELEUILLLEVALPHESETYRILLEPHMETPECYSER 20  
 DB 1 GGTGGAACTTCTGGCTTTCTCATCATGTTGTTTCTATATATACATGTTCTGTTCC 60  
 QY 21 ILEGINLYSTHRLALEUGINLTHRGIVUALARGASNCYSPHEGLYARGLUVALALA 40  
 DB 61 ATTCAAAAACCGCCTGCAGACACAGAGTAAGGAATGTTTGGAGAGAGGTGGCT 120  
 QY 41 VALAIAASNAARGPHEPHEILEVALPHESEASPALAILECYSTRIPLEPROVALPHE 60  
 DB 121 GTTGCAAAATCGTTCTTTTATAGTGTCTCGATGCCATGCTGGAGATTCCTGATATT 180  
 QY 61 VALVALLYSILEUSESERLEUPHEARGLVALGUILLEPROASPHMETHRISERTIPLE 80

DB 181 GYAGTTAAATCCTTTCCCTCCCGGGGAAATACAGACAAATGACTTCCTGGATA 240  
 QY 81 VALILEPHEPHEUPROVALASNSERATALEUASPROILLEUPTLRHLEUPRTTR 100  
 DB 241 GTGATTTTTCCTTCCAGTACAGTGTGTAATCCAACTCTATACCTCAGACACC 300  
 QY 101 ASNPHEPHELYSAPLYSLEU 107  
 DB 301 AACTTTTAAAGACAAAGTTG 321  
 RESULT 2  
 ABL40194  
 ID ABL40194 standard; cDNA; 1065 BP.  
 AC ABL40194;  
 XX  
 XX 23-MAY-2002 (first entry)  
 DT  
 XX  
 DE Human G protein-coupled receptor TGR17-4 encoding cDNA SEQ ID NO:11.  
 XX  
 XX Human; G protein-coupled receptor; TGR17-4; nootropic; antiinflammatory;  
 KW vasotropic; immunomodulator; cytostatic; gene therapy; protein therapy;  
 KW neurological; inflammatory; circulatory; degenerative; immune system;  
 KW digestive disease; cancer; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1065  
 FT /tag= a  
 FT /product= "TGR17-4"  
 FT /note= "no stop codon given"  
 FT  
 PN WO200204640-A1.  
 PD 17-JAN-2002.  
 XX  
 XX 06-JUL-2001; 2001WO-JP05878.  
 PF  
 XX 07-JUL-2000; 2000JP-0211989.  
 PR 18-DEC-2000; 2000JP-0383794.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Moriya T, Ito T, Shintani Y, Miyajima N;  
 DR  
 DR WPI: 2002-179706/23.  
 P-PSDB: ABB06253.  
 XX  
 PS Claim 7; Page 125-126; 145pp; Japanese.  
 XX  
 CC The present invention describes a human guanine nucleotide binding  
 CC protein (G protein) coupled receptor protein designated TGR17, which has  
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
 CC additional residues at the N-terminal. The TGR17 proteins have nootropic,  
 CC antiinflammatory, vasotropic, immunomodulator and cytostatic activities.  
 CC The TGR17 polynucleotides and protein can be used in gene therapy and  
 CC protein therapy. G-protein coupled receptor proteins are cell membrane  
 CC proteins mediating the cellular response to a large variety of signalling  
 CC molecules. The TGR17 polynucleotides and proteins can be used in the  
 CC diagnosis, treatment and prevention of diseases including neurological,  
 CC inflammatory, circulatory, degenerative, immune system and digestive  
 CC diseases and cancer. The present sequence encodes human TGR17-4 from the  
 CC present invention.  
 XX  
 SQ Sequence 1065 BP; 277 A; 214 C; 213 G; 361 T; 0 other;

## Alignment Scores:

Pred. No.: 1,47e-57 Length: 1065  
 Score: 549.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0

US-09-930-312-2 (1-107) x ABL40194 (1-1065)

QY 1 GlyValAsnLeuLeuAlaPheLeuIleIleValAlaPheSerTyrIleThrMetPheCysSer 20  
 DB 589 GGTTGAACACTGCTGCTTTTCATCATCATGTTTCCATATTAATTAATGTTCTGTTCC 648  
 QY 21 IleGlnLysThrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAla 40  
 DB 649 ATTCAAAAAACCCGCTTGACGACCAAGAGTAAGAAATGTTTGGAAAGAGTGCGCT 708  
 QY 41 ValAlaAsnArgPhePhePheIleValAlaPheSerAspAlaIleCysTyrPileProValPhe 60  
 DB 709 GTTGCAAAATCGTTCTTTTATAGTGTCTCTGATGCCATCTGCGATTCCTGATATT 768  
 QY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetIleThrPile 80  
 DB 769 GTGATTAAATCCTTCCCTTCCGCGTGGAATACCAACACAAATGACTTCTCGATA 828  
 QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuYrThrLeuThrThr 100  
 DB 829 GTGATTTTTTCTTCACAGTAACTGCTTTGAATCCAAATCTCTATTAATCTCACAACC 888  
 QY 101 AsnPhePheLysAspLysLeu 107  
 DB 889 AACTTTTAAAGCAAGTTG 909

## RESULT 3

AA507943

ID AA507943 standard; cDNA; 1068 BP.

XX AA507943;

XX 23-OCT-2001 (first entry)

XX Human cDNA encoding G-protein coupled receptor, hRUP16.

XX Human; G-protein coupled receptor; GPCR; hRUP16; agonist;

XX Inverse agonist; lung cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..1068

XX FT /tag= "a

XX FT /product= "hRUP16"

XX PD WO200136471-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000MO-US31509.

XX 17-NOV-1999; 9905-0166088.

XX 17-NOV-1999; 9905-0166099.

XX 23-DEC-1999; 9905-0171900.

XX 23-DEC-1999; 9905-0171901.

XX 23-DEC-1999; 9905-0171902.

XX 11-FEB-2000; 200005-0181749.

XX 14-MAR-2000; 200005-0189258.

XX 14-MAR-2000; 200005-0189259.

XX 10-APR-2000; 200005-0195898.

XX 10-APR-2000; 200005-0195899.

XX 10-APR-2000; 200005-0196078.

XX 28-APR-2000; 200005-0200419.

PR 12-MAY-2000; 200005-0203630.  
 PR 12-JUN-2000; 200005-0210741.  
 PR 12-JUN-2000; 200005-0210982.  
 PR 21-AUG-2000; 200005-0226760.  
 PR 26-SEP-2000; 200005-0235418.  
 PR 26-SEP-2000; 200005-0235779.  
 PR 20-OCT-2000; 200005-0242332.  
 PR 20-OCT-2000; 200005-0242343.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Lowitz KP;

XX MPI: 2001-355616/37.

XX P-PSDB: AAU04370.

XX Endogenous and non-endogenous versions of human G-protein coupled

XX receptors for direct identification of candidate compounds as agonists,

XX inverse agonists or partial agonists for use as therapeutic agents -

XX Claim 35; Page 104-105; 159pp; English.

XX The sequence encodes a human G-protein coupled receptor (GPCR),

XX hRUP16. The endogenous and non-endogenous, constitutively activated

XX versions of human G-protein coupled receptors (GPCR), are useful for

XX direct identification of candidate compounds as receptor agonists,

XX inverse agonists or partial agonists having applicability as therapeutic

XX agents for treating diseases related to GPCR, e.g. lung cancer.

XX Non-endogenous version of human GPCRs are also utilized in research

XX settings and in vitro and in vivo system, incorporating GPCRs can be

XX utilized to elucidate and understand the roles these receptors

XX play in the human condition, both normal and diseased.

XX SQ Sequence 1068 BP; 278 A; 215 C; 214 G; 361 T; 0 other;

## Alignment Scores:

Pred. No.: 1,47e-57 Length: 1068  
 Score: 549.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-09-930-312-2 (1-107) x AA507943 (1-1068)

QY 1 GlyValAsnLeuLeuAlaPheLeuIleIleValAlaPheSerTyrIleThrMetPheCysSer 20  
 DB 589 GGTTGAACACTGCTGCTTTTCATCATCATGTTTCCATATTAATTAATGTTCTGTTCC 648  
 QY 21 IleGlnLysThrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAla 40  
 DB 649 ATTCAAAAAACCCGCTTGACGACCAAGAGTAAGAAATGTTTGGAAAGAGTGCGCT 708  
 QY 41 ValAlaAsnArgPhePhePheIleValAlaPheSerAspAlaIleCysTyrPileProValPhe 60  
 DB 709 GTTGCAAAATCGTTCTTTTATAGTGTCTCTGATGCCATCTGCGATTCCTGATATT 768  
 QY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetIleThrPile 80  
 DB 769 GTGATTAAATCCTTCCCTTCCGCGTGGAATACCAACACAAATGACTTCTCGATA 828  
 QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuYrThrLeuThrThr 100  
 DB 829 GTGATTTTTTCTTCACAGTAACTGCTTTGAATCCAAATCTCTATTAATCTCACAACC 888  
 QY 101 AsnPhePheLysAspLysLeu 107  
 DB 889 AACTTTTAAAGCAAGTTG 909

## RESULT 4

ABL40192

ID ABL40192 standard; cDNA; 1473 BP.

```

AC ABL40192;
XX
XX 23-MAY-2002 (first entry)
DE Human G protein-coupled receptor TGR17-3 encoding cDNA SEQ ID NO:8.
XX
XX Human; G protein-coupled receptor; TGR17-3; neotropic; antiinflammatory;
XX vasotropic; immunomodulator; cytosstatic; gene therapy; protein therapy;
XX neurological; inflammatory; circulatory; degenerative; immune system;
XX digestive disease; cancer; gene; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1473
FT /*tag= a
FT /partial
FT /product= "TGR17-3"
FT /note= "no stop codon given"
XX
XX WO200204640-A1.
XX
XX 17-JAN-2002.
XX
XX 06-JUL-2001; 2001WO-JP05878.
XX
XX 07-JUL-2000; 2000JP-0211989.
XX 18-DEC-2000; 2000JP-0383794.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Moriya T, Ito T, Shintani Y, Miyajima N;
XX
XX WPI: 2002-179706/23.
XX P-PSDB; ABB06252.
XX
XX G-protein coupled receptor protein TGR17 of human origin and DNA
XX encoding it for diagnosis and treatment of cancer and circulatory and
XX other diseases associated with its expression -
XX
XX Claim 7; Page 122-123; 145pp; Japanese.
XX
XX The present invention describes a human guanine nucleotide binding
XX protein (G protein) coupled receptor protein designated TGR17, which has
XX 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having
XX additional residues at the N-terminal. The TGR17 proteins have neotropic,
XX antiinflammatory, vasotropic, immunomodulator and cytosstatic activities.
XX The TGR17 polynucleotides and protein can be used in gene therapy and:
XX protein therapy. G-protein coupled receptor proteins are cell membrane
XX proteins mediating the cellular response to a large variety of signalling
XX molecules. The TGR17 polynucleotides and proteins can be used in the
XX diagnosis, treatment and prevention of diseases including neurological,
XX inflammatory, circulatory, degenerative, immune system and digestive
XX diseases and cancer. The present sequence encodes human TGR17-3 from the
XX present invention.
XX
XX Sequence 1473 BP; 405 A; 310 C; 278 G; 480 T; 0 other;
XX
Alignment Scores:
Pred. No.: 2,23e-57 Length: 1473
Score: 549.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
XX
US-09-930-312-2 (1-107) x ABL40192 (1-1473)
OY 1 GlyValAsnLeuLeuAlaPheLeuIleValAlaPheSerTyrIlePheThrMetPheCysSer 20
DB 997 GGGTGAACCTGCTGCTTTTCATCATTTGTTTCCATATTTACTATNGTCTCTCC 1056
OY 21 TleGlnLysThrAlaLeuGlnThrGluValArgAsnCysPheGlyArgGluValAla 40

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DB 1057 ATTCAGAAAAACCGCCCTTCGACACACAGATGAGATTTGTTGAGAGAGGCGCT 1116
OY 41 ValAlaAsnArgPhePhePheIleValAlaPheSerAspAlaIleCysTrpIleProValPhe 60
DB 1117 GTTCGAAATCGCTTCTCTTTTATAGTGTCTCTGATGCCATCTCGATTCCTGATTTT 1176
OY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetPheSerTrpIle 80
DB 1177 GTAGTTAAATCCCTTCCCTCCGCGTGGAATACACAGACATGACTTCCTGTGATA 1236
OY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrIleuThrTr 100
DB 1237 GTGATTTTTCCTTCCTTCACATTAACAGTGTGAAACCAATCCTCTATCTCACACACC 1296
OY 101 AsnPhePheLysAspLysLeu 107
DB 1297 AACCTTTTAAAGCACAGTTG 1317
XX
XX RESULT 5
XX ABL40191
XX ID ABL40191 standard; cDNA; 1545 BP.
XX
XX ABL40191;
XX
XX 23-MAY-2002 (first entry)
XX
XX Human G protein-coupled receptor TGR17-2 encoding cDNA SEQ ID NO:6.
XX
XX Human; G protein-coupled receptor; TGR17-2; neotropic; antiinflammatory;
XX vasotropic; immunomodulator; cytosstatic; gene therapy; protein therapy;
XX neurological; inflammatory; circulatory; degenerative; immune system;
XX digestive disease; cancer; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1545
XX /*tag= a
XX /partial
XX /product= "TGR17-2"
XX /note= "no stop codon given"
XX
XX WO200204640-A1.
XX
XX 17-JAN-2002.
XX
XX 06-JUL-2001; 2001WO-JP05878.
XX
XX 07-JUL-2000; 2000JP-0211989.
XX 18-DEC-2000; 2000JP-0383794.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Moriya T, Ito T, Shintani Y, Miyajima N;
XX
XX WPI: 2002-179706/23.
XX P-PSDB; ABB06251.
XX
XX G-protein coupled receptor protein TGR17 of human origin and DNA
XX encoding it for diagnosis and treatment of cancer and circulatory and
XX other diseases associated with its expression -
XX
XX Claim 7; Page 118-119; 145pp; Japanese.
XX
XX The present invention describes a human guanine nucleotide binding
XX protein (G protein) coupled receptor protein designated TGR17, which has
XX 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having
XX additional residues at the N-terminal. The TGR17 proteins have neotropic,
XX antiinflammatory, vasotropic, immunomodulator and cytosstatic activities.
XX The TGR17 polynucleotides and protein can be used in gene therapy and
XX protein therapy. G-protein coupled receptor proteins are cell membrane
XX proteins mediating the cellular response to a large variety of signalling

```

PR 07-JUL-2000; 2000JP-0211989.

XX

DE cDNA encoding human G-protein coupled receptor HGPBMY5 splice variant.  
 XX Human; G-protein coupled receptor; GPCR; HGPBMY5; colon; brain;  
 KW ovary; thymus; lung; immune system; cancer; immune disorder;  
 KW neurological disorder; infection; human immunodeficiency virus; HIV;  
 KW antiallergic; antiaesthetic; dermatological; antiarteriosclerotic;  
 KW anticancer; antididiabetic; nephrotoxic; osteopathic; antiarthritic;  
 KW antiinflammatory; antirheumatic; antihypoid; cytostatic; vulnery;  
 KW virucide; antibacterial; antifungal; antiparasitic; protozoacide;  
 KW antihelmthic; nootropic; neuroprotective; antidepressant;  
 KW anticonvulsant; antiparkinsonian; neuroleptic; anti-HIV; gene; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 1..2142  
 FT /\*tag= a  
 FT /product= "GPCR HGPBMY5"  
 FT  
 FT MO200226824-A2.  
 XX  
 XX PD 04-APR-2002.  
 XX  
 XX PE 26-SEP-2001; 2001WO-US30365.  
 XX  
 XX PR 27-SEP-2000; 2000US-235713P.  
 XX PR 16-JAN-2001; 2001US-261781P.  
 XX PR 19-JUL-2001; 2001US-306605P.  
 XX PR 03-AUG-2001; 2001US-310436P.  
 XX  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 XX PI Feder JN, Mintier G, Ramanathan CS, Hawken DR;  
 DR WPI; 2002-435196/46.  
 DR P-PSDB; AAU97159.  
 XX  
 XX PT Novel G protein-coupled receptor, HGPBMY5 polypeptide, useful for  
 XX treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative  
 XX colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,  
 XX osteoarthritis  
 PS  
 PS Claim 1; Fig 5; 148pp; English.  
 CC  
 CC The present invention relates to the isolation of a novel human  
 CC G-protein coupled receptor (GPCR) (HGPBMY5), and the polynucleotide  
 CC sequence encoding it. The HGPBMY5 polypeptide and polynucleotide  
 CC are useful for preventing, treating or ameliorating a disease,  
 CC disorder or condition related to the colon, brain, ovaries, thymus,  
 CC lungs or immune system. They are particularly useful for the  
 CC treatment or prevention of cancers, immune disorders, neurological  
 CC disorders, and diseases related to the brain, ovaries, thymus or  
 CC lungs. The polynucleotide sequence is useful for diagnosing or  
 CC determining susceptibility to infections such as bacterial, fungal,  
 CC protozoan and viral infections, particularly infections caused by  
 CC human immunodeficiency virus (HIV or HIV-2). The present sequence  
 CC encodes a splice variant of human GPCR HGPBMY5.  
 XX  
 XX SO Sequence 2142 BP; 613 A; 435 C; 408 G; 686 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3.61e-57 Length: 2142  
 Score: 549.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-930-312-2 (1-107) x ABR51947 (1-2142)  
 OY 1 glyValAsnLeuLeuAlaPheLeuLeuIleValIlePheSerTyrIleThrMetPheCysSer 20  
 DB 1663 GGTTGGAAGTCTGCTGCTTTCTCATCATGTTCTTCTATATATCTATGTTCTGTTCC 1722

OY 21 IleGlnIysThrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAla 40  
 DB 1723 ATTCAAAAACCCGCTTGGACAGCACAGAAATGTTTGGAAAGAGGCGCT 1782  
 OY 41 ValAlaAsnArgPhePheIleValIlePheSerAspAlaIleCysTrpIleProValPhe 60  
 DB 1783 GTTGGAAACCGTCTTCTTTTATGAGTCTCTGATGCATCTGCTGGATTCGTATTT 1842  
 OY 61 ValValIysIleLeuSerLeuPheArgValIleIleProAspThrMetThrSerTrpIle 80  
 DB 1843 GTAGTTAAATCCTTCCCTCTCCGGTGGAAATACAGACACATGACTTCTGGATA 1902  
 OY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100  
 DB 1903 GTGATTTTTCCTCTCCATTAACAGTGTCTTGATTCACATCTCTCATACCTCACAACC 1962  
 OY 101 AsnPhePheLeuAspLysLeu 107  
 DB 1963 AACTTTTAAAGACAGATTG 1983  
 RESULT 8  
 ABL40197  
 ID ABL40197 standard; cDNA; 2190 BP.  
 XX  
 XX AC ABL40197;  
 XX  
 XX DT 23-MAY-2002 (first entry)  
 XX  
 XX DE Human G protein-coupled receptor TGR17-6 encoding cDNA SEQ ID NO:16.  
 XX  
 XX KW Human; G protein-coupled receptor; TGR17-6; nootropic; antiinflammatory;  
 KW vasotropic; immunomodulator; cytostatic; gene therapy; protein therapy;  
 KW neurological; inflammatory; circulatory; degenerative; immune system;  
 KW digestive disease; cancer; gene; ss.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX FH Key Location/Qualifiers  
 FT CDS 1..2190  
 FT /\*tag= a  
 FT /partial  
 FT /product= "TGR17-6"  
 FT /note= "no stop codon given"  
 FT  
 FT WO200204640-A1.  
 XX  
 XX PN 17-JAN-2002.  
 XX  
 XX PD 06-JUL-2001; 2001WO-JP05878.  
 XX  
 XX PR 07-JUL-2000; 2000JP-0211989.  
 XX PR 18-DEC-2000; 2000JP-0383794.  
 XX  
 XX PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX PI Moriya T, Ito T, Shintani Y, Miyajima N;  
 DR WPI; 2002-179706/23.  
 DR P-PSDB; ABB06255.  
 XX  
 XX PT G-protein coupled receptor protein TGR17 of human origin and DNA  
 XX encoding it for diagnosis and treatment of cancer and circulatory and  
 XX other diseases associated with its expression  
 PS  
 PS Claim 7; Page 135-136; 145pp; Japanese.  
 CC  
 CC The present invention describes a human guanine nucleotide binding  
 CC protein (G-protein) coupled receptor protein designated TGR17, which has  
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
 CC additional residues at the N-terminal. The TGR17 proteins have nootropic,  
 CC antiinflammatory, vasotropic, immunomodulator and cytostatic activities.  
 CC The TGR17 polynucleotides and protein can be used in gene therapy and

CC protein therapy. G-protein coupled receptor proteins are cell membrane  
CC proteins mediating the cellular response to a large variety of signaling  
CC molecules. The TGR17 polynucleotides and proteins can be used in the  
CC diagnosis, treatment and prevention of diseases including neurological,  
CC inflammatory, circulatory, degenerative, immune system and digestive  
CC diseases and cancer. The present sequence encodes human TGR17-6 from the  
CC present invention.

XX  
SQ Sequence 2190 BP; 626 A; 457 C; 409 G; 698 T; 0 other;

#### Alignment Scores:

Pred. No.:	3,72e-57	Length:	2190
Score:	549.00	Matches:	107
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-930-312-2 (1-107) x AB140197 (1-2190)

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OY 1 GlyValAsnLeuDeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer 20
DB 1714 GGGTGAACCTGCTGCTTTTCATCATGTTGTTTCTATATTAATGTTCTGTTCC 1773
OY 21 IleGlnLysThrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAla 40
DB 1774 ATTCAAAAACCCCTTGACACACAGAAAGTAAGAAATGTTTGGAAGAGAGGGCGCT 1833
OY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60
DB 1834 GTTGCAAAACGTTCTTTTAAAGTGTCTCGATGCCATCGCGATCTCTGATATT 1893
OY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetPheTrpIle 80
DB 1894 GTAGTTAAATCCTTTCCCTCTCCGGGAGAAATACACAGACATGACTTCTGATA 1953
OY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThr 100
DB 1954 GTGATTTTTTCTCCCTCACTAAGTGTGAAATCAATCCTATACTCTCACAAACC 2013
OY 101 AsnPhePheLysAspLysLeu 107
DB 2014 AACTTTTAAAGCAAGTTG 2034

RESULT 9
ABK51944
ID ABK51944 standard; cDNA; 2214 BP.
XX
AC ABK51944;
XX
DT 27-AUG-2002 (first entry)
XX
DE cDNA encoding human G-protein coupled receptor HGPRBM5.
XX
XX Human; G-protein coupled receptor; GPCR; HGPRBM5; colon; brain;
KW ovary; thymus; lung; immune system; cancer; immune disorder;
KW neurological disorder; infection; human immunodeficiency virus; HIV;
KW antiallergic; antihistaminic; dermatological; antiarteriosclerotic;
KW antitumor; antidiabetic; nephrotoxic; osteopathic; antiarthritic;
KW antiinflammatory; antipneumatic; antithyroid; cytostatic; vulnary;
KW virucide; antibacterial; antifungal; antiparasitic; protozoacide;
KW antihelminthic; nootropic; neuroprotective; antidepressant;
KW anticonvulsant; antiparkinsonian; neuroleptic; anti-HIV; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2214
FT /tag= a
FT /product= "GPCR HGPRBM5"
XX
XX W0200226824-A2.
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PD 04-APR-2002.

XX 26-SEP-2001; 2001WO-US30365.

XX 27-SEP-2000; 2000US-235713P.

PR 16-JAN-2001; 2001US-261781P.

PR 19-JUL-2001; 2001US-306605P.

PR 03-AUG-2001; 2001US-310436P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Feder JN, Mintler G, Ramanathan CS, Hawken DR;

XX WPI; 2002-435196/46.

DR P-PSDB; AAU97158.

PT Novel G protein-coupled receptor, HGPRBM5 polypeptide, useful for

PT treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative

PT colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,

PT osteoarthritis

XX Claim 1: Fig 1; 148pp; English.

XX The present invention relates to the isolation of a novel human

CC G-protein coupled receptor (GPCR) (HGPRBM5), and the polynucleotide

CC sequence encoding it. The HGPRBM5 polypeptide and polynucleotide

CC are useful for preventing, treating or ameliorating a disease,

CC disorder or condition related to the colon, brain, ovaries, thymus,

CC lungs or immune system. They are particularly useful for the

CC treatment or prevention of cancers, immune disorders, neurological

CC disorders, and diseases related to the brain, ovaries, thymus or

CC lungs. The polynucleotide sequence is useful for diagnosing or

CC determining susceptibility to infections such as bacterial, fungal,

CC protozoan and viral infections, particularly infections caused by

CC human immunodeficiency virus (HIV or HIV-2). The present sequence

CC encodes human GPCR HGPRBM5.

XX

SQ Sequence 2214 BP; 638 A; 457 C; 416 G; 703 T; 0 other;

XX

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

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US-09-930-312-2 (1-107) x ABK51944 (1-2214)

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OY 21 IleGlnLysThrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAla 40
DB 1795 ATTCAAAAACCCCTTGACACACAGAAAGTAAGAAATGTTTGGAAGAGAGGGCGCT 1854
OY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60
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OY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetPheTrpIle 80
DB 1915 GTAGTTAAATCCTTTCCCTCTCCGGGAGAAATACACAGACATGACTTCTGATA 1974
OY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThr 100
DB 1975 GTGATTTTTTCTCCCTCACTAAGTGTGAAATCAATCCTATACTCTCACAAACC 2034
OY 101 AsnPhePheLysAspLysLeu 107
DB 2035 AACTTTTAAAGCAAGTTG 2055
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 AC ABL40196;  
 XX  
 XX 23-MAY-2002 (first entry)  
 DT  
 DE Human G protein-coupled receptor TGR17-5 encoding cDNA seq ID NO:14.  
 XX  
 KW Human: G protein-coupled receptor; TGR17-5; nocitropic; antinflammatory;  
 KW vasotropic; immunomodulator; cytostatic; gene therapy; protein therapy;  
 KW neurological; inflammatory; circulatory; degenerative; immune system;  
 KW digestive disease; cancer; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2262  
 FT /\*tag= a  
 FT /partial  
 FT /product= "TGR17-5"  
 FT /note= "no stop codon given"  
 XX  
 PM WO200204640-A1.  
 PD 17-JAN-2002.  
 XX  
 PF 06-JUL-2001; 2001WO-JP05878.  
 XX  
 PR 07-JUL-2000; 2000JP-0211989.  
 PR 18-DEC-2000; 2000JP-0383794.  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Moriya T, Ito T, Shintani Y, Miyajima N;  
 XX  
 DR WPI: 2002-179706/23.  
 XX  
 DR P-PSDB: ABB06254.  
 PT G-protein coupled receptor protein TGR17 of human origin and DNA  
 PT encoding it for diagnosis and treatment of cancer and circulatory and  
 PT other diseases associated with its expression -  
 XX  
 PS Claim 7; Page 130-131; 145pp; Japanese.  
 XX  
 CC The present invention describes a human guanine nucleotide binding  
 CC protein (G protein) coupled receptor designated TGR17, which has  
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having  
 CC additional residues at the N-terminal. The TGR17 proteins have nocitropic,  
 CC antinflammatory, vasotropic, immunomodulator and cytostatic activities.  
 CC The TGR17 polynucleotides and protein can be used in gene therapy and  
 CC protein therapy. G-protein coupled receptor proteins are cell membrane  
 CC proteins mediating the cellular response to a large variety of signalling  
 CC molecules. The TGR17 polynucleotides and proteins can be used in the  
 CC diagnosis, treatment and prevention of diseases including neurological,  
 CC inflammatory, circulatory, degenerative, immune system and digestive  
 CC diseases and cancer. The present sequence encodes human TGR17-5 from the  
 CC present invention.  
 XX  
 SQ Sequence 2262 BP; 650 A; 467 C; 421 G; 724 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3.88e-57 Length: 2262  
 Score: 549.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-930-312-2 (1-107) x ABL40196 (1-2262)  
 QY 1 GlyValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer 20

|||||  
 Db 1786 GGTGTGAACCTTCGTGCTTCTTCATCATCTGTGTTCCTATATACATGTTCTGTTCC 1845  
 QY 21 IIEGLNLSYTHRALeudInThrThrcIuValArgAsnCysPheGLYArgGLuValAla 40  
 Db 1846 ATTCAAAAAACCCGCTTCGACACCCAGAGTAGAGAAATGTTTGGAGAGAGAGGTGGCT 1905  
 QY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60  
 Db 1906 GTTCGAAATCGTTCTTTTATAGTGTCTCTGATGCCATCGTGGATTCCTGATTT 1965  
 QY 61 ValValLSIleLeuSerIleuPheArgValGLuIleProAsPThMetHserTrpIle 80  
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 AC AAI99584;  
 XX  
 DT 04-JAN-2002 (first entry)  
 XX  
 DE Human expressed polynucleotide SEQ ID NO 47.  
 XX  
 KW Human: nocitropic; neuroprotective; cytostatic; dermatological; virucide;  
 KW immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary;  
 KW antiparkinsonian; antisticking; antianaemic; antiarthritic; cancer;  
 KW antirheumatic; hepatotropic; cerebroprotective; antinflammatory;  
 KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;  
 KW antiparasitic; cardiatic; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine;  
 ss.  
 OS Homo sapiens.  
 XX  
 PM WO200155387-A1.  
 PD 02-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US01310.  
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 PR 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
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 PR 18-APR-2000; 2000US-0198123.  
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PR 20-OCT-2000; 2000US-0241808.  
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PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
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PR 17-NOV-2000; 2000US-0249299.  
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PR 11-DEC-2000; 2000US-0251990.  
PR 05-JAN-2001; 2000US-0254097.  
PR 05-JAN-2001; 2000US-0259678.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI: 2001-451937/48.  
DR P-PSDB; ABB04062.  
DR  
XX  
XX  
XX Isolated polypeptide for treating, preventing and/or prognosing  
PT disorders related to the musculoskeletal system including  
PT musculoskeletal cancers and also for testing and detection e.g.  
PT diagnosis -  
PS  
XX Claim 1: SEQ ID NO 986; 781pp + Sequence Listing; English.  
XX  
XX The invention relates to novel genes (AAL34669-AAL37666) and proteins  
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful  
CC for preventing, treating or ameliorating medical conditions e.g. by  
CC protein or gene therapy. The genes are isolated from a range of human  
CC tissues disclosed in the specification. The nucleic acids, proteins,  
CC antibodies and (ant)agonists are useful in the diagnosis, treatment

CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and  
CC other cancers of the adrenal gland, bone, bone marrow, breast,  
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound  
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;  
CC and (f) infectious diseases such as viral, bacterial, fungal and  
CC parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
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Percent Similarity: 83.18% Conservative: 20  
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DB: 22 Gaps: 0  
  
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Db 92 GTTCATCAAGTGCATATACAGCAAGCACTGAATACGATCAAGTTAAAGAGATGATC 151  
  
QY 41 ValAlaAsnArghPhePhePheIleValPheSerAspAlaIleCysTPrIleProValPhe 60  
Db 152 CTGGCAACAGTTTCTTTCTTTATATATATCTAGTATGATGATGATGATGATGATGAT 211  
  
QY 61 ValValIysIleLeuSerLeuPheArgValGluIleProAspThrMetThSerTrpIle 80  
Db 212 GTAGTGAATTTCTTTCCTGCTGCTTACGATACCAATACAGTACCATACCTTTGGGTA 271  
  
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100  
Db 272 GTGATTTTATTCGCCATTAACAGTCTTTGAACCAATTCCTATATCTGATCAGCA 331  
  
QY 101 AsnPhePheIysAspIysLeu 107  
Db 332 AGACCATTTAAAGAAATGATT 352  
  
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XX  
XX  
AC ABA06471;  
XX  
DT 10-JAN-2002 (first entry)  
XX  
DE Human cDNA SEQ ID NO: 137.  
XX  
XX Human; gene therapy; neural disorder; immune system disorder;  
XX muscular disorder; reproductive disorder; gastrointestinal disorder;  
XX pulmonary disorder; cardiovascular disorder; renal disorder;  
XX proliferative disorder; inflammation; SS.  
OS Homo sapiens.  
XX  
XX W0200154474-A2.  
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XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01349.  
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PR 05-DEC-2000; 2000US-251030P.  
PR 05-DEC-2000; 2000US-251988P.  
PR 05-DEC-2000; 2000US-256719P.  
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PR 08-DEC-2000; 2000US-251868P.  
PR 08-DEC-2000; 2000US-251869P.  
PR 08-DEC-2000; 2000US-251989P.  
PR 08-DEC-2000; 2000US-251990P.  
PR 11-DEC-2000; 2000US-254097P.  
PR 05-JAN-2001; 2001US-259678P.  
  
(HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI: 2001-476161/51.  
DR P-PSDB: ABB10249.  
XX  
XX  
PT

Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical

PT condition  
XX  
PS Claim 1; SEQ ID NO: 137; 859pp + Sequence Listing; English.  
XX  
CC The present invention provides human cDNAs, proteins and related genomic  
CC DNAs. These can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence  
CC is a cDNA of the invention.  
XX  
SQ Sequence 530 BP; 158 A; 105 C; 95 G; 171 T; 1 other;  
  
Alignment Scores:  
Pred. No.: 8,34e-37 Length: 530  
Score: 376.00 Matches: 69  
Percent Similarity: 83.188 Conservative: 20  
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Db 32 GGTATTAAATTTGGCCGCGCATTCATCATGATTTTCCATGGAACGATGTTTATAGT 91  
QY 21 IleGlyLysThrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAla 40  
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QY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60  
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Db 212 GTAGTGAATTTCTTCCACGCTTACGTTAGTAACATACAGGTAACCTCTTGGGTA 271  
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100  
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Db 272 GTGATTTTATTCTGCCCATTAACAGTCTTTGACCCCAATCTCTACTCTGACACACA 331  
QY 101 AsnPhePheLysAspIlyLeu 107  
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XX  
XX AAS28950;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
XX  
DE cDNA encoding for human uterine motility-association polypeptide #15.  
XX  
KM Human; uterine motility-association disorder; uterus; pregnancy;  
XX labour; menstrual cycle; gene therapy; ss.  
OS Homo sapiens.  
XX  
PN WO200155201-A1.  
XX  
PD 02-AUG-2001.  
XX  
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PR 31-JAN-2000; 2000US-0179065.  
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PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0253676.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI: 2001-48877/53.  
XX P-PSDB; AAU18108.  
XX  
XX Isolated polypeptide and nucleic acid molecules for treating,  
XX preventing and/or prognosing disorders related to uterine motility  
XX e.g. disorders associated with pregnancy and the menstrual cycle -  
XX  
XX  
XX Claim 4: SEQ ID No 25; 524pp; English.  
XX  
XX The present invention relates to the isolation of novel human  
XX uterine motility-association polypeptides (AAU18094-AAU18152),

CC and cDNA and genomic sequences encoding for these polypeptides.  
CC The sequences of the invention are useful in the diagnosis,  
CC treatment, prevention and/or prognosis of diseases associated  
CC with uterine motility such as pregnancy and labour, and menstrual  
CC disorders. The polynucleotide sequences of the invention are also  
CC useful in gene therapy. AAS28936-AAS28994 represent cDNA sequences  
CC encoding for novel human uterine motility-association polypeptides.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).  
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Score: 376.00 Matches: 69  
Percent Similarity: 83.18% Conservative: 20  
Best Local Similarity: 64.49% Mismatches: 18  
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QY 21 IleGlnLysThrAlaLeuGlnThrGluValAlaGAsnCysPheGlyArgGluValAla 40  
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QY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTyrIleProValPhe 60  
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XX cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;  
XX ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;  
XX hyperproliferative disorder; breast; liver; cardiovascular disorder; ss;  
XX cerebrovascular disorder; nervous system disorder; bacterial infection;  
XX fungal infection; viral infection; ocular disorder; endocrine disorder;  
XX gastrointestinal disorder; renal disorder; respiratory disorder;  
XX wound healing; skin aging; organ transplantation; food preservative;  
XX tissue regeneration; anti-infertility.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX  
XX PN WO20015364-A2.  
XX

PD 02-AUG-2001.  
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PF 17-JAN-2001; 2001MO-US01308.  
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(HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Rosen CA, Barash SC, Ruben SM;  
PI  
XX WPI; 2001-451936/48.  
DR





GenCore version 5.1.4.p5.4578  
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# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 26, 2003, 20:05:47 ; Search time 52 Seconds  
(without alignments)  
631.046 Million cell updates/sec

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Perfect score: 549  
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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	138.5	25.2	2987	4	US-07-757-342D-1
4	125	22.8	1298	4	US-08-795-876-32
5	125	22.8	1300	4	US-08-795-876-31
6	125	22.8	1300	4	US-08-795-876-36
7	125	22.8	1300	4	US-08-795-876-37
8	125	22.8	2179	1	US-08-487-886-1
9	125	22.8	2179	2	US-08-531-070A-1
10	125	22.8	2179	3	US-08-482-855-1
11	125	22.8	2179	4	US-08-474-986-1
12	123	22.4	981	1	US-08-349-696-20

13	123	22.4	981	1	US-08-233-009-20	Sequence 20, Appl
14	123	22.4	981	1	US-08-560-231-20	Sequence 20, Appl
15	123	22.4	981	4	US-09-080-704A-20	Sequence 20, Appl
16	123	22.4	2180	1	US-07-918-314-3	Sequence 3, Appl
17	123	22.4	2900	1	US-07-918-314-5	Sequence 5, Appl
18	120.5	21.9	4417	4	US-07-741-453A-57	Sequence 57, Appl
19	119.5	21.8	957	1	US-08-349-696-26	Sequence 26, Appl
20	119.5	21.8	957	1	US-08-233-009-26	Sequence 26, Appl
21	119.5	21.8	957	1	US-08-560-231-26	Sequence 26, Appl
22	119.5	21.8	957	4	US-09-080-704A-26	Sequence 26, Appl
23	119.5	21.8	3710	4	US-07-741-453A-62	Sequence 62, Appl
24	116	20.9	1859	1	US-08-293-563-1	Sequence 1, Appl
25	115	20.9	999	1	US-08-349-696-24	Sequence 24, Appl
26	115	20.9	999	1	US-08-233-009-24	Sequence 24, Appl
27	115	20.9	999	1	US-08-560-231-24	Sequence 24, Appl
28	115	20.9	999	4	US-09-080-704A-24	Sequence 24, Appl
29	109	19.9	473	2	US-08-866-757-3	Sequence 3, Appl
30	109	19.9	473	4	US-09-153-593-3	Sequence 3, Appl
31	109	19.9	4203	2	US-08-866-757-1	Sequence 1, Appl
32	109	19.9	4203	4	US-09-153-593-1	Sequence 1, Appl
33	108	19.7	1205	1	US-08-417-103-13	Sequence 13, Appl
34	108	19.7	1265	1	US-07-816-283-3	Sequence 3, Appl
35	108	19.7	1265	1	US-08-417-103-3	Sequence 3, Appl
36	108	19.7	1634	1	US-07-816-283-1	Sequence 1, Appl
37	108	19.7	1634	1	US-08-417-103-1	Sequence 1, Appl
38	105	19.1	1149	4	US-09-262-477-1	Sequence 1, Appl
39	103.5	18.9	2862	1	US-08-148-209A-1	Sequence 1, Appl
40	103.5	18.9	2884	1	US-08-148-209A-5	Sequence 5, Appl
41	102.5	18.7	1639	1	US-08-334-698-5	Sequence 5, Appl
42	102.5	18.7	1639	1	US-08-228-932-5	Sequence 5, Appl
43	102.5	18.7	1639	1	US-08-468-853-5	Sequence 5, Appl
44	102.5	18.7	1639	2	US-08-406-855A-5	Sequence 5, Appl
45	102.5	18.7	1639	2	US-08-722-190-5	Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-08-101-435-3  
Sequence 3, Application US/08101435  
Patent No. 5441883  
GENERAL INFORMATION:  
APPLICANT: Civealli, Olivier  
TITLE OF INVENTION: A No. 5441883el Adenosine Receptor and Uses  
CORRESPONDENCE ADDRESS: 7  
ADDRESS: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/101,435  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/847,563  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 91,708  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317



```
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2987 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2097
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-07-757-342D-1

Alignment Scores:
Pred. No.: 7,35e-08 Length: 2987
Score: 138.50 Matches: 29
Percent Similarity: 51.92% Conservative: 25
Best Local Similarity: 27.88% Mismatches: 43
Query Match: 25.23% Indels: 7
Gaps: 2

DB:
US-09-930-312-2 (1-107) x US-07-757-342D-1 (1-2987)
QY 2 ValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrlleThrMetPheCysSerIle 21
Db 1600 CTCGAATGCTGGCGCTTCATTAATTTGCTTGCCTGCTACATTAATAATTTATTTGCAAGT 1659
QY 22 GlnIysThrAlaLeuGlnThrGluValAlaArgsnCysPheGlyArgGluValAlaVal 41
Db 1660 CGAAGACCCAGAAATTAATGCTACC-----AAATGAAGATCAAGAAATTT 1701
QY 42 AlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPheVal 61
Db 1702 GCTAAGAAATGGCAATCCATCTTCACCGATTTTCACGACGACGACCATCTCTTT 1761
QY 62 ValIysIleLeuSerLeuPheArgValGlu--IleProAspThrMetThrSerTrpIle 80
Db 1762 TTGGCCATCTCAGCTCCATCAAGATCCTTATCACAGTAACCACTCAAGATTTTA 1821
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrlleThrLeuThr 100
Db 1822 CTGGTTCTTTTATTCATCAATCTTGTGGCAATCATTCTGTATGCAATATTTCACT 1881
QY 101 AsnPhePheIys 104
Db 1882 AAGACATTCACA 1893

RESULT 4
US-08-795-876-32/c
; Sequence 32, Application US/08795876
; Patent No. 6403305
GENERAL INFORMATION:
APPLICANT: Gershengorn, Marvin C.
APPLICANT: Geras-Raaka, Elizabeth
TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
```

```
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,876
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-795-876-32

Alignment Scores:
Pred. No.: 1,21e-06 Length: 1298
Score: 125.00 Matches: 28
Percent Similarity: 52.83% Conservative: 28
Best Local Similarity: 26.42% Mismatches: 42
Query Match: 22.77% Indels: 8
Gaps: 3

DB:
US-09-930-312-2 (1-107) x US-08-795-876-32 (1-1298)
QY 2 ValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrlleThrMetPheCysSerIle 21
Db 486 CTCGAATGCTGGCGCTTCATTAATTTGCTTGCCTGCTACATTAATAATTTATTTGCAAGT 427
QY 22 GlnIysThrAlaLeuGlnThrGluValAlaArgsnCysPheGlyArgGluValAlaVal 41
Db 426 CGGAACCCAGCAATGCTCTCC-----TCTAGTGAACACACGAGATC 385
QY 42 AlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPheVal 61
Db 384 GCCAAGGCGCATGCGATCTTCATCTGACTTCTGCTGACATGGACCCATTTCTTTC 325
QY 62 ValIysIleLeuSerLeuPheArgValGlu--IleProAspThrMetThrSerTrpIle 80
Db 324 TTGGCCATTTCTGCTCCCTCAAGAGTCCCTCATCACTGTGTCAAAGCAAGATTCGT 265
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrlleThrLeuThr 99
Db 264 CTGGTTCTGTTTCAACCCATCACTCTGTGCAACCCCTTCTGTATGCAATCTTAAAC 205
QY 100 ThrAsnPhePheIysAsp 105
Db 204 AAAAATCTTGCAGAGAT 187

RESULT 5
US-08-795-876-31
; Sequence 31, Application US/08795876
; Patent No. 6403305
GENERAL INFORMATION:
APPLICANT: Gershengorn, Marvin C.
APPLICANT: Geras-Raaka, Elizabeth
TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN
```



US-08-795-876-37/c  
; Sequence 37, Application US/08795876  
; Patent No. 6403305  
; GENERAL INFORMATION:  
; APPLICANT: Gershengorn, Marvin C.  
; APPLICANT: Geras-Raaka, Elizabeth  
; APPLICANT: Nussenzweig, Daniel R.  
; TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN  
; NUMBER OF INVENTION: COUPLED RECEPTORS  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,876  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BRAMAN, SUSAN J.  
; REGISTRATION NUMBER: 34,103  
; REFERENCE/DOCKET NUMBER: 19603/1280  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 716-263-1636  
; TELEFAX: 716-263-1600  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1300 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-795-876-37  
Alignment Scores:  
Pred. No.: 1.22e-06 Length: 1300  
Score: 125.00 Matches: 28  
Percent Similarity: 52.83% Conservative: 28  
Best Local Similarity: 26.42% Mismatches: 42  
Query Match: 22.77% Indels: 8  
DB: Gaps: 3  
US-09-930-312-2 (1-107) x US-08-795-876-37 (1-1300)  
QY 2 ValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSerIle 21  
DB 486 CTCGAATGCTCTGCGCTTGTGGTCATCTGCTGCTATATCCACATCACTCAACAGTG 427  
QY 22 GlnLysThAlaLeuGlnThrTgIuValArgAsnCysPheGlyArgGluValAlaVal 41  
DB 426 CGGAACCCCAACATCTGCTCTCC-----TCTAGTGCACCCAGATC 385  
QY 42 AlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPheVal 61  
DB 384 GCCAAGCCGATGGCCATGCTCATCTTCACTGCTCTGCTGCATGGCACCACATTTCTTC 325  
QY 62 ValLysIleLeuSerIleuPheArgValGlu---IleProAspThrMetThrSerTrpIle 80  
DB 324 TTTGCATTTCCTGCGCTCCCTCAAGGTGCCCTCATCTGCTGCCAAGCAAGATTCG 265  
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuYrThrIleu---Thr 99  
DB 264 CTGGTCTCTTTCACCCCACTCAACTCTCTGCTGCACACCCCTTCTTATGCACTTTTACC 205  
QY 100 ThrAsnPhePheLysasp 105

DB 204 AAAAATTGCGACAGAT 187  
RESULT 8  
US-08-487-886-1  
; Sequence 1, Application US/08487886  
; Patent No. 5744448  
; GENERAL INFORMATION:  
; APPLICANT: Kelton, Christie Ann  
; APPLICANT: Schweickhardt, Rene Lynn  
; APPLICANT: Cheng, Shirley Vui Yen  
; APPLICANT: Nugent, No. 5744448een Patrice  
; TITLE OF INVENTION: Human Follicle Stimulating  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Stephan P. Williams,  
; ADDRESSEE: Ares-Serono, Inc.  
; STREET: Exchange Place, 37th floor  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density  
; COMPUTER: IBM PS/2, model 55 SX  
; OPERATING SYSTEM: MS-DOS version 4.0  
; SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,886  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/670,085  
; FILING DATE: 15-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Stephan P.  
; REGISTRATION NUMBER: 28546  
; REFERENCE/DOCKET NUMBER: US/252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 723-1300  
; TELEFAX: (617) 723-8923  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2179  
; TYPE: Nucleic acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; TISSUE TYPE: Testis  
; IMMEDIATE SOURCE:  
; LIBRARY: 19c11 cDNA library, Clontech #HL1010B  
; CLONE: pHFSHR11-11, pHFSHR15-6  
; FEATURE:  
; NAME/KEY: protein coding region  
; LOCATION: 75 to 2159  
; US-08-487-886-1  
Alignment Scores:  
Pred. No.: 2.39e-06 Length: 2179  
Score: 125.00 Matches: 28  
Percent Similarity: 52.83% Conservative: 28  
Best Local Similarity: 26.42% Mismatches: 42  
Query Match: 22.77% Indels: 8  
DB: Gaps: 3  
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QY 2 ValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSerIle 21  
DB 1683 CTCGAATGCTCTGCGCTTGTGGTCATCTGCTGCTATATCCACATCACTCAACAGTG 1742

Qy 22 GlnLysThrAlaLeuGlnThrGluValArgAsnCysPheGlyArgGluValAlaVal 41  
 Db 1743 CGGAACCCCAACATGTCCTCC-----TCTAGTACACCCAGATC 1784  
 Qy 42 AlaAsnArgPhePhePheValValPheSerAspAlaIleCysTrpIleProValPheVal 61  
 Db 1785 GCCAAGCCCATGGCCATCATCTTCACTGACTTCTCTGCATGGACACCATTTCTTTC 1844  
 Qy 62 ValLysIleLeuSerLeuPheArgValGlu---IleProAspThrMetThrSerTrpIle 80  
 Db 1845 TTGGCATTTTCGCTCCCTCAAGTGGCCCTCATCATCTGTCCTCAAGCAAGATTTCTG 1904  
 Qy 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyThrLeu---Thr 99  
 Db 1905 CTGGTTCGTTTCACCCCATCAACCTCCTGTCACCAACCTTCTCTATGCCATCTTTACC 1964  
 Qy 100 ThrAsnPhelPheLysAsp 105  
 Db 1965 AAAAAGTTTCGCGAGAT 1982

## RESULT 9

US-08-531-070A-1  
 ; Sequence 1, Application US/08531070A :  
 ; Patent No. 5851768  
 ; GENERAL INFORMATION:  
 ; APPLICANT: de la Chapelle, Albert  
 ; APPLICANT: Altomaki, Kristina  
 ; APPLICANT: Huhtaniemi, Ilpo  
 ; TITLE OF INVENTION: Method for Diagnosis of Ovarian Dysgenesis  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/531.070A  
 ; FILING DATE: 20-SEP-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Gass, David A.  
 ; REGISTRATION NUMBER: 38,153  
 ; REFERENCE/DOCKET NUMBER: 28113/32879  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312/474-6300  
 ; TELEFAX: 312/474-0448  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2179 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-531-070A-1

## Alignment Scores:

Pred. No.: 2,39e-06 Length: 2179  
 Score: 125.00 Matches: 28  
 Percent Similarity: 52.83% Conservative: 28  
 Best Local Similarity: 26.42% Mismatches: 8  
 Query Match: 22.77% Indels: 2  
 DB: 2 Gaps: 3

US-09-930-312-2 (1-107) x US-08-531-070A-1 (1-2179)

Qy 2 ValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrlleThrMetPheCysSerile 21  
 Db 1683 CTCATGTCCTGCTGCTTTGTGTCATCTGTGCTGATATCATCATCTACCTCAGAG 1742  
 Qy 22 GlnLysThrAlaLeuGlnThrGluValArgAsnCysPheGlyArgGluValAlaVal 41  
 Db 1743 CGGAACCCCAACATGTCCTCC-----TCTAGTACACCCAGATC 1784  
 Qy 42 AlaAsnArgPhePhePheValValPheSerAspAlaIleCysTrpIleProValPheVal 61  
 Db 1785 GCCAAGCCCATGGCCATCATCTTCACTGACTTCTCTGCATGGACACCATTTCTTTC 1844  
 Qy 62 ValLysIleLeuSerLeuPheArgValGlu---IleProAspThrMetThrSerTrpIle 80  
 Db 1845 TTGGCATTTTCGCTCCCTCAAGTGGCCCTCATCATCTGTCCTCAAGCAAGATTTCTG 1904  
 Qy 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyThrLeu---Thr 99  
 Db 1905 CTGGTTCGTTTCACCCCATCAACCTCCTGTCACCAACCTTCTCTATGCCATCTTTACC 1964  
 Qy 100 ThrAsnPhelPheLysAsp 105  
 Db 1965 AAAAAGTTTCGCGAGAT 1982

## RESULT 10

US-08-482-855-1  
 ; Sequence 1, Application US/08482855  
 ; Patent No. 6121016  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kelton, Christie Ann  
 ; APPLICANT: Schweickhardt, Rene Lynn  
 ; APPLICANT: Cheng, Shirley Vui Yen  
 ; APPLICANT: Nugent, No. 6121016een Patrice  
 ; TITLE OF INVENTION: Hormone Receptor  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Stephan P. Williams,  
 ; STREET: Exchange Place, 37th floor  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density  
 ; COMPUTER: IBM PS/2, model 55 SX  
 ; OPERATING SYSTEM: MS-DOS version 4.0  
 ; SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/482.855  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/670,085  
 ; FILING DATE: 15-MAR-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Williams, Stephan P.  
 ; REGISTRATION NUMBER: 28546  
 ; REFERENCE/DOCKET NUMBER: US/252  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 723-1300  
 ; TELEFAX: (617) 723-8923  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2179  
 ; TYPE: Nucleic acid  
 ; STRANDEDNESS: Double  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens

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: TISSUE TYPE: Testis
: IMMEDIATE SOURCE:
: LIBRARY: Ig11 cDNA library, Clontech #HL1010b
: CLONE: pFHSR11-11, pFHSR15-6
: FEATURE:
: NAME/KEY: protein coding region
: LOCATION: 75 to 2159
: US-08-482-855-1

Alignment Scores:
Pred. No.: 2,39e-06 Length: 2179
Score: 125.00 Matches: 28
Percent Similarity: 52.83% Conservative: 28
Best Local Similarity: 26.42% Mismatches: 42
Query Match: 22.77% Indels: 8
DB: 3 Gaps: 3

US-09-930-312-2 (1-107) x US-08-482-855-1 (1-2179)
QY 2 ValasnleuLeuAlaPheLeuIleValPheSerTyrlleThrmPheCysSerile 21
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1683 CTCATATGCTGCGCTTGGTGTGATCTGTGGCTGATATACCATCTACTACAGTG 1742
QY 22 GlnLysThrAlaLeuGlnThrGluValArgAsnCysPheGlyArgGluValAlaVal 41
: ||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 1743 CGGAACCCCAACATCGTGTCTCC-----TCTAGTACACACAGATC 1784
QY 42 AlaSnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPheVal 61
: ||| ||| |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 1785 GCCAAGCGCATGCGCATCTCTTCATCTGCTGATGCGACCCATTTCTTTC 1844
QY 62 ValLysIleLeuSerLeuPheArgValGlu--IleProAspThrMetThrSerTrpIle 80
: ||| ||| |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 1845 TTTCCTATTTCTGCTCCCTCCCAAGTGCCCTCATCTGTCGCAAGCAAGATTCGTG 1904
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrlleu---Thr 99
: |||||: ||| |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 1905 CTGTTCTGTTTCACCATCACTCCTGTGCCACCCCTTCCTATGCACTTTTACC 1964
QY 100 ThrAsnPhePheLysasp 105
: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 1965 AAAAATTTCGACAGAT 1982

RESULT 11
US-08-474-986-1
: Sequence 1, Application US/08474986
: Patent No. 6372711
: GENERAL INFORMATION:
: APPLICANT: Kelton, Christie Ann
: Schewelchardt, Rene Lynn
: Cheng, Shirley Vui Yen
: Nugent, No. 6372711leen Patrice
: TITLE OF INVENTION: Human Follicle Stimulating
: Hormone Receptor
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Stephan P. Williams,
: Ares-Serono, Inc.
: STREET: Exchange Place, 37th floor
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
: COMPUTER: IBM PS/2, model 55 SX
: OPERATING SYSTEM: MS-DOS version 4.0
: SOFTWARE: VAX/VMS Massill via Kermit to IBM MS-DOS
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/474,986
: FILING DATE: 07-Jun-1995
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: 07/670,085
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams, Stephan P.
: REGISTRATION NUMBER: 28546
: REFERENCE/DOCKET NUMBER: US/252
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 723-1300
: TELEFAX: (617) 723-8923
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2179
: TYPE: Nucleic acid
: STRANDEDNESS: Double
: TOPOLOGY: Linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: TISSUE TYPE: Testis
: IMMEDIATE SOURCE:
: LIBRARY: Ig11 cDNA library, Clontech #HL1010b
: CLONE: pFHSR11-11, pFHSR15-6
: FEATURE:
: NAME/KEY: protein coding region
: LOCATION: 75 to 2159
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
: US-08-474-986-1

Alignment Scores:
Pred. No.: 2,39e-06 Length: 2179
Score: 125.00 Matches: 28
Percent Similarity: 52.83% Conservative: 28
Best Local Similarity: 26.42% Mismatches: 42
Query Match: 22.77% Indels: 8
DB: 4 Gaps: 3

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QY 22 GlnLysThrAlaLeuGlnThrGluValArgAsnCysPheGlyArgGluValAlaVal 41
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Db 1743 CGGAACCCCAACATCGTGTCTCC-----TCTAGTACACACAGATC 1784
QY 42 AlaSnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPheVal 61
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Db 1785 GCCAAGCGCATGCGCATCTCTTCATCTGCTGATGCGACCCATTTCTTTC 1844
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Db 1845 TTTCCTATTTCTGCTCCCTCCCAAGTGCCCTCATCTGTCGCAAGCAAGATTCGTG 1904
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QY 100 ThrAsnPhePheLysasp 105
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Db 1965 AAAAATTTCGACAGAT 1982

RESULT 12
US-08-349-696-20
: Sequence 20, Application US/08349696
: Patent No. 559671
: GENERAL INFORMATION:
: APPLICANT: Jacobson, Marlene A
: APPICANT: Johnson, Robert G
: APPLICANT: Luneau, Christopher J
: APPLICANT: Salvatore, Christopher A
: TITLE OF INVENTION: Human Adenosine Receptors
: NUMBER OF SEQUENCES: 28

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: United States
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh IIfx
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,696
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: us/08/005945
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 186991A
TELEPHONE: (908)594-4678
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-349-696-20

Alignment Scores:
Pred. No.: 1,5e-06 Length: 981
Score: 123.00 Matches: 29
Percent Similarity: 52.88% Conservative: 26
Best Local Similarity: 27.88% Mismatches: 41
Query Match: 22.40% Indels: 8
DB: 1 Gaps: 3

US-09-930-312-2 (1-107) x US-08-349-696-20 (1-981)
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Db 580 CTCCTCATGTCCTCTCTACCTGAGGCTCTTCTACTTACCGCAAGCAGCTCAGCAAG 639
QY 23 LysThrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAlaValAla 42
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QY 43 AsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPheValVal 62
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QY 63 LysIleLeuSerLeuPhe-----ArgValGluIleProAspThrMetThrSerTrpIle 80
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QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrIleuThrThr 100
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RESULT 13
US-08-233-009-20
; Sequence 20, Application US/08233009
; Patent No. 3646156
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GENERAL INFORMATION:
APPLICANT: Jacobson, Marlene A
APPLICANT: Johnson, Robert G
APPLICANT: Salvatore, Christopher A
TITLE OF INVENTION: INHIBITION OF EOSINOPHIL
TITLE OF INVENTION: ACTIVATION THROUGH A3 ADENOSINE RECEPTOR ANTAGONISM
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESS: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,009
FILING DATE: 25-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Benzen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19219
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3901
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-233-009-20

Alignment Scores:
pred. No.: 1,5e-06 Length: 981
Score: 123.00 Matches: 29
Percent Similarity: 52.88% Conservative: 26
Best Local Similarity: 27.88% Mismatches: 41
Query Match: 22.40% Indels: 8
DB: 1 Gaps: 3

US-09-930-312-2 (1-107) x US-08-233-009-20 (1-981)
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Db 580 CTCCTCATGTCCTCTCTACCTGAGGCTCTTCTACTTACCGCAAGCAGCTCAGCAAG 639
QY 23 LysThrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAlaValAla 42
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Db 640 AAGGTCTCGCCCTCTCCGCGCGCAGAGTACTATGGAAGAGAGCTGAGAGATCGCC 699
QY 43 AsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPheValVal 62
Db 700 AAGTCGCTGGCCCTCATCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
QY 63 LysIleLeuSerLeuPhe-----ArgValGluIleProAspThrMetThrSerTrpIle 80
Db 760 AACTGATCATCCCTCTTTCGCCGCTCTGCGCAGACCCAGCATCTTACC---TACATT 816
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrIleuThrThr 100
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QY 101 AsnPhePheLys 104
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; Sequence 20, Application US/09080704A
; Patent No. 6166181
; GENERAL INFORMATION:
; APPLICANT: Jacobson, Marlene A
; APPLICANT: Johnson, Robert G
; APPLICANT: Luneau, Christopher J
; APPLICANT: Salvatore, Christopher A
; TITLE OF INVENTION: Human Adenosine Receptors
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: United States
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080.704A
; FILING DATE: 18 May 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Parr, Richard S.
; REGISTRATION NUMBER: 32,586
; REFERENCE/DOCKET NUMBER: 18699DB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)594-4958
; TELEFAX: (732)594-4720
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-080-704A-20

Alignment Scores:
Pred. No.: 1.5e-06 Length: 981
Score: 123.00 Matches: 29
Percent Similarity: 52.88% Conservative: 26
Best Local Similarity: 27.88% Mismatches: 41
Query Match: 22.40% Indels: 8
DB: 4 Gaps: 3

US-09-930-312-2 (1-107) x US-09-080-704A-20 (1-981)
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Db      580  CTCCTCAGTCGCTCCATCTACTCTGAGAGTCTTCTACTACTATCCGCAAGCAGCTTCACACAG 639
QY      23  LysThrAlaLeuGlnThrThrGluValArgAsnCysPheGlyArgGluValAlaValAla 42
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Db      640  AAGGTGTCGGCTCTCCGCGAGCCCGCAGAGTACTGTGGAAGGAGCGAAGATCCGCC 699
QY      43  AsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPheValAla 62
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Db      700  AAGTCGCTGCGCCCTTCATCTCTTCTCTTGCCCTTCAGCTGGCGCTTGCGACATCTCTC 759
QY      63  LysIleLeuSerIleAlaPhe-----ArgValGluIleProAspThrMetTrpSerTrpIle 80
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Wed May 28 08:38:10 2003

us-09-930-312-2.rni

Page 10

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Qy 101 AsnIephpeIyIs 104 .

Db 877 CAGAGATTCCGC 888

Search completed: May 26, 2003, 21:21:13  
Job time : 59 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 26, 2003, 20:08:08 : Search time 155 Seconds  
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911.545 Million cell updates/sec

Title: US-09-930-312-2

Perfect score: 549

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-O=/cg2n\_1/USPTO.spool/US09930312/runat.22052003.114615.27125/app.query.fasta.1.263  
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-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications\_NA.\*

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12: /cg2n\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
13: /cg2n\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cg2n\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	100.0	321	9	US-09-930-312-1
2	549	100.0	2049	10	US-09-928-175-11
3	549	100.0	2142	9	US-09-965-536A-5
4	549	100.0	2193	10	US-09-928-175-6

5	549	100.0	2214	9	US-09-965-536A-1	Sequence 1, Appl1
6	549	100.0	2265	10	US-09-928-175-1	Sequence 1, Appl1
7	549	100.0	2436	9	US-10-229-735-2	Sequence 2, Appl1
8	549	100.0	2838	9	US-10-222-668-1	Sequence 1, Appl1
9	478	87.1	2214	10	US-09-928-175-19	Sequence 19, Appl1
10	478	87.1	2539	9	US-10-229-735-4	Sequence 4, Appl1
11	376	68.5	530	9	US-09-989-442-33	Sequence 33, Appl1
12	376	68.5	530	9	US-10-073-865-25	Sequence 25, Appl1
13	376	68.5	530	9	US-10-103-313-89	Sequence 89, Appl1
14	376	68.5	530	10	US-09-764-833-137	Sequence 137, App
15	376	68.5	530	10	US-09-764-877-986	Sequence 986, App
16	376	68.5	1804	10	US-09-895-668-10	Sequence 10, Appl1
17	371	67.6	612	10	US-09-895-666-37	Sequence 37, Appl1
18	371	67.6	1018	9	US-09-782-974C-65	Sequence 65, Appl1
19	234	42.6	1015	9	US-10-270-333-20	Sequence 20, Appl1
20	225	41.0	1080	9	US-10-270-333-26	Sequence 26, Appl1
21	225	41.0	3187	9	US-10-270-333-25	Sequence 25, Appl1
22	181	33.0	3574	9	US-10-270-333-19	Sequence 19, Appl1
23	149.5	27.2	432	10	US-09-895-668-62	Sequence 62, Appl1
24	142	25.9	2586	10	US-09-804-551B-19	Sequence 5, Appl1
25	138.5	25.2	2100	10	US-09-804-626-5	Sequence 1, Appl1
26	136.5	24.9	2902	10	US-09-877-804-1	Sequence 7, Appl1
27	125	22.8	2088	10	US-09-804-626-7	Sequence 4, Appl1
28	123	22.4	1942	9	US-09-800-274-1	Sequence 1, Appl1
29	123	22.4	3349	9	US-10-270-336-4	Sequence 4, Appl1
30	122	22.2	2366	10	US-09-877-804-5	Sequence 5, Appl1
31	120	21.9	2487	9	US-10-270-336-1	Sequence 1, Appl1
32	120	21.9	3438	9	US-10-176-847-89	Sequence 89, Appl1
33	120	21.9	119596	9	US-10-270-336-3	Sequence 3, Appl1
34	119.5	21.8	1739	9	US-09-800-274-3	Sequence 3, Appl1
35	118.5	21.6	2512	9	US-10-045-624B-1	Sequence 1, Appl1
36	113	20.6	572	9	US-09-925-299-296	Sequence 296, App
37	113	20.6	572	10	US-09-925-299-296	Sequence 296, App
38	109	19.9	2703	10	US-09-984-271-75	Sequence 75, Appl1
39	109	19.9	2714	9	US-09-925-299-202	Sequence 202, App
40	109	19.9	2714	10	US-09-925-299-202	Sequence 124, App
41	109	19.9	3429	9	US-09-822-846-124	Sequence 1, Appl1
42	109	19.9	3688	10	US-09-862-767A-1	Sequence 34626, A
43	105	19.1	422	9	US-09-918-995-34626	Sequence 2, Appl1
44	105	19.1	1032	9	US-09-971-228-2	Sequence 14, Appl1
45	105	19.1	1089	10	US-09-993-844-14	

## ALIGNMENTS

RESULT 1  
US-09-930-312-1  
; Sequence 1, Application US/09930312  
; Publication No. US20030032019A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia & Upjohn Company  
; APPLICANT: Lind, Peter  
; TITLE OF INVENTION: No. US20030032019A1el G Protein-Coupled Receptors  
; FILE REFERENCE: 00329, PCT1  
; CURRENT APPLICATION NUMBER: US/09/930,312  
; PRIOR FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: USSN 60/225,262  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-930-312-1

Alignment Scores:  
Pred. No.: 2.89e-61 Length: 321  
Score: 549.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Gaps: 0  
DB: 9



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Db	1903	GTGATTTTTTTCCTCCAGTTAAACAGTGGCTTTGAATCCATCCTATCTCACAACC	1962
Qy	101	AsnPhePheLysAspLysLeu	107
Db	1963	AACTTTTTTTAAAGCACAGTTG	1983

## RESULT 4

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US-09-928-175-6
: Sequence 6, Application US/09928175
: Patent No. US20020123618A1
: GENERAL INFORMATION:
: APPLICANT: Paszly, Christopher J.
: APPLICANT: Gong, Jianhua
: APPLICANT: Daugherty, Betsy
: APPLICANT: Rogers, No. US20020123618A1ma
: TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
: FILE REFERENCE: 00-1229
: CURRENT APPLICATION NUMBER: US/09/928,175
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: 60/224,455
: PRIOR FILING DATE: 2000-08-10
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 2193
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(2190)
: NAME/KEY: sig_peptide
: LOCATION: (1)..(108)
: US-09-928-175-6

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**Alignment Scores:**

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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Qy	21	IleGlnIysThrAlaLeuGlnThrThrgluValaIArgAsnCysPheGlyArgGluValaAla	40
Db	1774	ATTCAAAAAACCGCCTTGCAGACCACAGAAAGTAAAGAAATGTTTGTGGAAGAAAGGTGGCT	1833
Qy	41	ValAlaAsnArgPhePhePheIleValaPheSerAspAlaIleCysTrpIleProValaPhe	60
Db	1834	GTTCAACATCGTTCTTTTATAGTGTCCTCGATGCATCGCTGCGATTCCTGATATT	1893
Qy	61	ValValIysIleLeuSerIleuPheArgValaGluIleProAspPheMetThrSerTrpIle	80
Db	1894	GTAATTAATAATCTTTTCCCTCTTCCGGGGTGGAAATACAGACACATGACTTCCTGGGATA	1953

QY	81	Val	Ile	Phe	Leu	Pro	Val	Asn	Ser	Ala	Ile	Asn	Pro	Ile	Leu	Tyr	Thr	Leu	Thr	Thr	100																														
Db	1954	G	T	G	A	T	T	T	T	T	T	C	C	T	T	C	A	G	T	T	A	C	A	G	T	G	C	T	T	T	G	A	T	C	C	A	T	C	T	T	A	C	T	C	T	C	A	C	A	C	2013

Qy	101	Asn	phe	ph	lys	asp	lys	leu	107
Db	2014	AACTTTT	TTTAAG	GACAC	AGTTC				2034

RESULT 5  
US-09-965-536A-1

US-09-965-536A-1

```

; Sequence 1, Application US/09965536A
; Publication No. US20030027323A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HANKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBWMY5
; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
; FILE REFERENCE: D0041NP
; CURRENT APPLICATION NUMBER: US/09/965,536A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2214
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-965-536A-1

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Alignment Scores:

Pred. No.:	4,47e-60	Length:	2214
Score:	549.00	Matches:	107
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-930-312-2 (1-107) x US-09-965-536A-1 (1-2214)

QY	1	GIYValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer	20
Db	1735	GGTGGAACTGCTGGCGCTTTCATCATCATGTCCTTCCATATTCATATGTCGTTCC	1794
QY	21	ITLeGlnyStrAlaIleuGlnThrThrGluValArgAsnCysPheGlyArgGluAla	40
Db	1795	ATTCAAAAACCGCTTCGACACACACAGAAAGTAAGATGTTTGGAGAAAGGCGT	1854
QY	41	ValAlaAsnATGPhenPhePheIleValPheSerAspAlaIleCysTrpIleProValPhe	60
Db	1855	GTTCGAATCTCTTCTTTTATATAGTGTCTCTGATGCCATCTGCTGGATTCTGTATTT	1914
QY	61	ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetThrSerTrpIle	80
Db	1915	GTAGTTAAATCTTTCCTTCCTTCCTCCGGGTGAATACACAGACATGACTTCCTGGATA	1974
QY	81	ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr	100
Db	1975	GTGATTTTTTTCCTTCCAGTTAAACAGTGGCTTGAATCCATCTCTATCTCCACACC	2034
QY	101	AsnPhenPheLysAspLysIleu	107
Db	2035	AACTTTTTAAAGACAAGTTG	2055

## RESULT 6

```

US-09-928-175-1
; Sequence 1, Application US/09928175
; Patent No. US20020123618A1
;
; GENERAL INFORMATION:
; APPLICANT: Paszly, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618A1ma
; TITLE OF INVENTION: Leucine-Rich G Protein
; TITLE OF INVENTION: Uses Thereof

```

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; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2265
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2262)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(108)
US-09-928-175-1

Alignment Scores:
Pred. No.: 4,61e-60 Length: 2265
Score: 549.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 10

US-09-930-312-2 (1-107) x US-09-928-175-1 (1-2265)

QY 1 GIYValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer 20
DB 1786 GGTGGAACCTGCTGGCTTTCTCATCATGTTCTTCTATATATACATGTTCTGTTCC 1845

QY 21 IIEGlnLysThrAlaLeuGlnThrThrgluValArgAsnCysPheGlyArgGluValAla 40
DB 1846 ATTCAAAAACCGCCTTCGAGACACAGAACTAAGCAATGTTTGGAGAGAGGTGCT 1905

QY 41 VALAlaAsnArgPhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60
DB 1906 GTTGCAAAATCGTTCTTTTATAGTGTCTGTGATGCCATCGCTGGATCTCGATT 1965

QY 61 VALValLysIleLeuSerLeuPheArgValGluIleProAspThrMetThrSerTrpIle 80
DB 1966 GTAGTTAAATCTTCTCCCTTCGCGGGTGAATACGACACACATGACTCTCGAT 2025

QY 81 VALIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100
DB 2026 GGATTTTTCCTTCCTCCAGTTAACAGTGTGTAATCCATCTATCTCTCACAAAC 2085

QY 101 AsnPhelLysAspLysLeu 107
DB 2086 AACCTTTTAAAGCACAGTTG 2106

RESULT 7
; Sequence 2, Application US/10/229735
; Publication No. US20030082650A1
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; APPLICANT: Agoulalik, Alexander I.
; TITLE OF INVENTION: The GREAT Gene and Protein
; FILE REFERENCE: 7572/73263
; CURRENT APPLICATION NUMBER: US/10/229,735
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/315,696
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/351,432
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
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```
US-10-229-735-2

Alignment Scores:
Pred. No.: 5,11e-60 Length: 2436
Score: 549.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

US-09-930-312-2 (1-107) x US-10-229-735-2 (1-2436)

QY 1 GIYValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer 20
DB 1856 GGTGGAACCTGCTGGCTTTCTCATCATGTTCTTCTATATATACATGTTCTGTTCC 1915

QY 21 IIEGlnLysThrAlaLeuGlnThrThrgluValArgAsnCysPheGlyArgGluValAla 40
DB 1916 ATTCAAAAACCGCCTTCGAGACACAGAACTAAGCAATGTTTGGAGAGAGGTGCT 1975

QY 41 VALAlaAsnArgPhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60
DB 1976 GTTGCAAAATCGTTCTTTTATAGTGTCTGTGATGCCATCGCTGGATCTCGATT 2035

QY 61 VALValLysIleLeuSerLeuPheArgValGluIleProAspThrMetThrSerTrpIle 80
DB 2036 GTAGTTAAATCTTCTCCCTTCGCGGGTGAATACGACACACATGACTCTCGAT 2095

QY 81 VALIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100
DB 2096 GGATTTTTCCTTCCTCCAGTTAACAGTGTGTAATCCATCTATCTCTCACAAAC 2155

QY 101 AsnPhelLysAspLysLeu 107
DB 2156 AACCTTTTAAAGCACAGTTG 2176

RESULT 8
; Sequence 1, Application US/10/222668
; Publication No. US2003008884A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Sheau Yu
; APPLICANT: Hsueh, Aaron
; TITLE OF INVENTION: Mammalian Relaxin Receptor
; FILE REFERENCE: STAN-239 WO
; CURRENT APPLICATION NUMBER: US/10/222,668
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/313,259
; PRIOR FILING DATE: 2002-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (107)..(2369)
US-10-222-668-1

Alignment Scores:
Pred. No.: 6,35e-60 Length: 2838
Score: 549.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

US-09-930-312-2 (1-107) x US-10-222-668-1 (1-2838)

QY 1 GIYValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer 20
DB 1892 GGTGGAACCTGCTGGCTTTCTCATCATGTTCTTCTATATATACATGTTCTGTTCC 1951
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APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: P1208  
CURRENT APPLICATION NUMBER: US/09/989,442  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/214,886  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/217,487  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,758  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,963  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/217,496  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,447  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/218,290  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/225,757  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/226,868  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/216,647  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,267  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/216,880  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,270  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/251,869  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/235,834  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/234,274  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/234,223  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/228,924  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/224,518  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,369  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/224,519  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,964  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/241,809  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/249,299  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/236,327  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/241,785  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/244,617  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 60/225,268  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,368  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/251,856  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/251,868  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/229,344  
PRIOR FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 60/234,997  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: 60/229,343  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,345  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,287  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,513  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/231,413  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/229,509  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/236,367  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/237,039  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,038  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/236,370  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/236,802  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,037  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,040  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/240,960  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/239,935  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/239,937  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/241,787  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,474  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/246,532  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/249,216  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,210  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/226,681  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,759  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/225,213  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/227,182  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,214  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/235,836  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/230,438  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/215,135  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/225,266  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/249,218  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,208  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,213  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,212  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,207  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,245



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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

```

## Alignment Scores:

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Pred. No.: 6,42e-39 Length: 530
Score: 376.00 Matches: 69
Percent Similarity: 83.18% Conservative: 20
Best Local Similarity: 64.49% Mismatches: 18
Query Match: 68.49% Indels: 0
DB: 9 Gaps: 0

```

US-09-930-312-2 (1-107) x US-09-989-442-33 (1-530)

```

QY 1 GlyValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer 20
   |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 32 GGTATTAAATTTGGCCCATTTATCATCATAGTTTTCCTATGCAAGCATGTTTATAGT 91
QY 21 IleGlnLysThrAlaLeuGlnThrGluValArgAsnCysPheGlyArgGluValAla 40
   ::|:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 92 GTTCATCAAGTGCATACAGCACTGAATACGGAATCAAGTAAAGAGATGATC 151
QY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60
   ::|:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 152 CTTGCCAAACGTTTCTTATAGTATTACTGATGATGATGATGATGATGATGATGATGAT 211

```

```

QY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetTrpSerTrpIle 80
   |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 212 GTAGTGAATTTCTTTCACAGCTTCACAGTGAATACAGTACAGTACAGTACAGTACAGT 271
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100
   |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 272 GTGATTTTATTCGCCATTAACAGTGTGTAACCAATTCCTATACTCTGACACACA 331
QY 101 AsnPhePheLysAspLysLeu 107
   |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 332 AGACCATTTAAAGAAATGATT 352

```

## RESULT 12

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US-10-073-865-25
; Sequence 25, Application US/10073865
; Publication No. US20030044904A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1209C1
; CURRENT APPLICATION NUMBER: US/10/073,865
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION REMOVED - See file Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ. ID NO. 25
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-073-865-25

```

## Alignment Scores:

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Pred. No.: 6,42e-39 Length: 530
Score: 376.00 Matches: 69
Percent Similarity: 83.18% Conservative: 20
Best Local Similarity: 64.49% Mismatches: 18
Query Match: 68.49% Indels: 0
DB: 9 Gaps: 0

```

US-09-930-312-2 (1-107) x US-10-073-865-25 (1-530)

```

QY 1 GlyValAsnLeuLeuAlaPheLeuIleIleValPheSerTyrIleThrMetPheCysSer 20
   |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 32 GGTATTAAATTTGGCCCATTTATCATCATAGTTTTCCTATGCAAGCATGTTTATAGT 91
QY 21 IleGlnLysThrAlaLeuGlnThrGluValArgAsnCysPheGlyArgGluValAla 40
   ::|:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 92 GTTCATCAAGTGCATACAGCACTGAATACGGAATCAAGTAAAGAGATGATC 151
QY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60
   ::|:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 152 CTTGCCAAACGTTTCTTATAGTATTACTGATGATGATGATGATGATGATGATGATGAT 211
QY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetTrpSerTrpIle 80
   |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 212 GTAGTGAATTTCTTTCACAGCTTCACAGTGAATACAGTACAGTACAGTACAGTACAGT 271
QY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100
   |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 272 GTGATTTTATTCGCCATTAACAGTGTGTAACCAATTCCTATACTCTGACACACA 331
QY 101 AsnPhePheLysAspLysLeu 107
   |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 332 AGACCATTTAAAGAAATGATT 352

```

## RESULT 13

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US-10-103-313-89
; Sequence 89, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

```



Db 272 GTGATTTTATCTGCCCATTACAGTGTGTAACCCAAATCTCTATACCTGACCACA 331  
QY 101 AsnPhelYsAsplysieu 107  
|||||:::  
Db 332 AGACCAATTTAAGAAATGATT 352

Search completed: May 26, 2003, 21:24:03  
Job time : 162 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.4 p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 26, 2003, 20:03:57 ; Search time 1716 Seconds

(without alignments) 1009.858 Million cell updates/sec

Title: US-09-930-312-2

Perfect score: 549

Sequence: 1 GVNLALFLIVFSYITMCS.....NSALNPILYLTITNFKDKL 107

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame\_plus\_p2n.model -DEV=xlh  
-Q/cgn2.1/USPTO/US09930312/runat\_22052003\_114614\_27077/app-query.fasta.1.263  
-DB=EST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -DOOPCL=0 -DOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR.SCORE=PCPT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NOM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09930312\_6CGN.1.1.1906\_@runat\_22052003\_114614\_27077 -NCPu=6 -ICPU=3  
-NO\_XLPPX -NO\_MAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120  
-WARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST :  
1: em\_estba :  
2: em\_estlum :  
3: em\_estlin :  
4: em\_estmu :  
5: em\_estov :  
6: em\_estpl :  
7: em\_estro :  
8: em\_hlc :  
9: gb\_est1 :  
10: gb\_est2 :  
11: gb\_hlc :  
12: gb\_est3 :  
13: gb\_est4 :  
14: gb\_est5 :  
15: em\_estlum :  
16: em\_estum :  
17: gb\_gss :  
18: em\_gss\_hum :  
19: em\_gss\_inv :  
20: em\_gss\_pln :  
21: em\_gss\_vrt :  
22: em\_gss\_fun :  
23: em\_gss\_mam :  
24: em\_gss\_mus :  
25: em\_gss\_other :  
26: em\_gss\_pro :  
27: em\_gss\_rtd :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	375	68.3	744	12 BG304121	BG304121 f130f05.x
2	361	65.8	841	12 BQ228832	BQ228832 AGENCOURT
3	316	57.6	197	12 BF942735	BF942735 EST-CD15N
4	288	52.5	235	10 AW436170	AW436170 75600 MAR
5	162	29.5	456	12 BF021857	BF021857 uy58h08.y
6	162	29.5	574	12 BB632810	BB632810 BB632910
7	142	25.9	573	13 B1630907	B1630907 RH60250.5
8	142	25.9	610	13 B1628622	B1628622 RH57122.5
9	137.5	25.0	511	14 BM960298	BM960298 c1h4L114S
10	137.5	25.0	522	10 AV995043	AV995043 AV995043
C 11	137.5	25.0	585	10 AV883650	AV883650 AV883650
12	132.5	24.1	676	10 BB553437	BB553437 BB553437
13	132.5	24.1	1113	13 BM454054	BM454054 AGENCOURT
14	132.5	24.1	1142	13 BM461149	BM461149 AGENCOURT
15	127.5	23.2	2372	11 AK013534	AK013534 Mus muscu
16	126	23.0	568	13 B1608244	B1608244 RH12435.5
17	126	23.0	2360	11 AK016635	AK016635 Mus muscu
18	125	22.8	548	12 BF075894	BF075894 225322 MA
19	124	22.6	935	17 CNS01M4J	AL150468 Anopheles
20	123	22.4	896	14 BQ225080	BQ225080 AGENCOURT
21	123	22.4	973	12 BG423878	BG423878 602449840
22	123	22.4	975	14 BQ958975	BQ958975 AGENCOURT
23	123	22.4	981	12 BG168804	BG168804 602320111
24	123	22.4	982	12 BF159363	BF159363 621770339
C 25	122	22.2	563	14 BM962037	BM962037 c1h4L114T
C 26	120.5	21.9	613	10 BE179105	BE179105 RC0-HT061
C 27	120.5	21.9	1101	17 CENS0181F	AL108765 Drosophila
C 28	120	21.9	655	12 BE985448	BE985448 UI-M-CGDP
29	118.5	21.6	3015	11 AK014519	AK014519 Mus muscu
30	117	21.3	518	10 AW660289	AW660289 98243 MAR
C 31	116.5	21.2	1050	17 CENS04V9T	AL308810 Tetradon
C 32	115	20.9	592	14 BM783394	BM783394 K-EST061
C 33	115	20.9	669	10 AW367357	AW367357 MR0-HT016
C 34	115	20.9	704	14 BM722841	BM722841 UI-E-EJ0-
35	115	20.9	786	12 BG2022798	BG2022798 RST22165
C 36	115	20.9	985	9 AL571416	AL571416 AL571416
C 37	114.5	20.9	885	17 CENS030UT	AL222734 Tetradon
38	113.5	20.7	528	14 BQ667379	BQ667379 pb60e12.y
39	113	20.6	510	12 BF516393	BF516393 UI-H-BW1-
40	112	20.4	571	14 BM741294	BM741294 K-EST0013
41	112	20.4	589	14 BM751805	BM751805 K-EST0028
42	112	20.4	928	9 AL545857	AL545857 AL545857
C 43	112	20.4	944	9 AL576349	AL576349 AL576349
C 44	112	20.4	1002	9 AL576584	AL576584 AL576584
45	111.5	20.3	538	13 BM130064	BM130064 pb26a08.y

#### ALIGNMENTS

RESULT 1  
LOCUS BG304121/c  
DEFINITION f130f05.x1 Sugano Kawakami zebrafish DRA Danio rerio cDNA clone  
3815552.3' similar to TR:Q9VBFO Q9VBFO CS5042 PROTEIN. ;, mRNA  
ACCESSION BG304121  
VERSION BG304121.1 GI:13101648  
KEYWORDS EST.  
SOURCE zebrafish.  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes  
; Cyprinidae; Danio.  
REFERENCE 1 (bases 1 to 744)

**AUTHORS**  
Sugano, S., Kawakami, K., Johnson, S., Li, F., Marra, M., Eddy, S., Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T., Mattlin, J., Pape, D., Steptoe, M., Underwood, R., Theising, B., Ritter, E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R.

**JOURNAL**  
Washu zebrafish EST project 1999  
Unpublished (1999)

**COMMENT**  
Contact: S.L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu

**FEATURES**  
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov  
Seq primer: 17 from Glbco  
High quality sequence stop: 510.

**SOURCE**  
Location/Qualifiers  
1..744  
/organism="Danio rerio"  
/strain="AB"  
/db\_xref="taxon:7955"  
/clone="3815552"  
/clone\_lib="Sugano Kawakami zebrafish DNA"  
/sex="mixed (one male and one female, including unfertilized eggs)"  
/dev\_stage="adult"  
/lab\_host="DH10B (phage resistant)"  
/note="Vector: pME18-FL3; Site\_1: DraIII (CAGCTGTG); Site\_2: DraIII (CAGCTGTG); 1st strand cDNA was primed with an oligo(dT) primer (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TTGTGGCTGTG), digested and cloned into distinct DraIII sites of the pME18-FL3 vector (5' site CAGCTGTG, 3' site CAGCTGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCGCTCTTAAGCTGCG and 3' end primer CGAGCTGAGCTGAGACA."

**BASE COUNT**  
204 a 158 c 186 g 196 t

**ORIGIN**

**Alignment Scores:**

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.8e-34	375.00	744	71	18	18	0	
Percent Similarity:	83.18%						
Best Local Similarity:	66.36%						
Query Match:	68.31%						

US-09-930-312-2 (1-107) x BG304121 (1-744)

OY 1 GYValAAsnLeuLeuAlaPheLeuIleValPheSerTyrIleThrMetPheCysSer 20  
DB 738 GGACTTACCCGGCTTCTTCATCGTGGTCTTCATCGACATGTTTACTTCC 679

OY 21 IlegInLysThAlaLeuGlnThrThrguValArgAsnCysPheGlyArgGluValAla 40  
DB 678 ATCTATAGACGGGATGAGACCCACAGACGCGGCGGTCCGACCTCACAGACGTTGCC 619

OY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60  
DB 618 ATGGCACACCGGCTTCTTCATCGTGGTTCATGCGCTTGTGATTCATTC 559

OY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetThSerTrpIle 80  
DB 558 ATGGTCAAAATCTCTCTTAATGAGGAGATACAGACGATCATCATCTTGGGTG 499

OY 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThr 100

DB 498 GTGATCTTCATCTCCCATCATCAAGAGCTGCTTAAGCCATCTTTACACACTGACAC 439

OY 101 AsnPhenelyAspLysLeu 107  
DB 438 AGTTTTTCAGAGACAGGTG 418

**RESULT 2**  
BQ228832  
LOCUS  
DEFINITION  
BQ228832 841 bp mRNA linear EST 02-MAY-2002  
AGENCOURT\_7522585 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6051251  
5', RNA sequence.

**ACCESSION**  
BQ228832  
VERSION  
BQ228832.1 GI:20410232  
KEYWORDS  
EST.

**SOURCE**  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

**REFERENCE**  
1 (bases 1 to 841)  
NIH-MGC http://mhc.ncl.nih.gov/  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs@femail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: L1AM1304 Row: m Column: 12  
High quality sequence start: 87  
High quality sequence stop: 603.

**FEATURES**  
Location/Qualifiers  
1..841  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6051251"  
/clone\_lib="NIH\_MGC\_72"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

**BASE COUNT**  
240 a 160 c 170 g 269 t 2 others

**ORIGIN**

**Alignment Scores:**

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1.89e-32	361.00	841	68	21	18	1	
Percent Similarity:	82.41%						
Best Local Similarity:	62.96%						
Query Match:	65.76%						

US-09-930-312-2 (1-107) x BQ228832 (1-841)

OY 1 GYValAAsnLeuLeuAlaPheLeuIleValPheSerTyrIleThrMetPheCysSer 20  
DB 335 GGTATTATTGGCCGCAATTATCATAGTTTTCCTATGAGACATGTTTATAGT 394

OY 21 IlegInLysThAlaLeuGlnThrThrguValArgAsnCysPheGlyArgGluValAla 40  
DB 395 GTTCTCAAAAGTGCATTAACAGCACTGAATAGCATCAAGTAAAGAGATGATC 454

OY 41 ValAlaAsnArgPhePhePheIleValPheSerAspAlaIleCysTrpIleProValPhe 60  
DB 455 GTTGCAAACGTTTCTTATATATATCTGATGATCATGCTGATATCCATTTT 514

OY 61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetThSerTrpIle 80

```

Db 515 GTAGTGAATTTCTTCTTCACTGCTTACAGTAGAATAACAGTACATACCTCTTGAGTA 574
Qy 81 ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrrHrleu-Thrth 100
Db 575 GTATTTTATTTATTTGTCCTTACAGTGTTCGACCAATCTTATCTGTAACCCA 634
Qy 100 rAsnPhePheLeuAspLysLeu 107
Db 635 AGACCATTTTAAAGAAATGAT 656

RESULT 3
BF942735 197 bp mRNA linear EST 15-SEP-2001
LOCUS EST-CD15N-040 human CD15+ myeloid progenitor cells cDNA library
DEFINITION Homo sapiens CDNA 3', mRNA sequence.
ACCESSION BF942735.1 GI:15624134
VERSION BF942735.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 197)
AUTHORS Chen,J., Lee,S., Zhou,G., Rowley,J.D. and Wang,S.M.
TITLE A high-throughput GLGI procedure for converting large number of
JOURNAL SAGE tag sequences into 3' ESTs
COMMENT Unpublished (2001)
CONTACT: Wang SM
Hem/Onc
University of Chicago Medical Center
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 773-702-6788
Fax: 773-702-3002
Email: swang@lemdway.uchicago.edu
This EST fragment was amplified from human CD15+ myeloid progenitor
cells cDNA library with GLGI technique (Generation of Longer cDNA
fragments from SAGE tags for Gene Identification, Proc. Natl. Acad.
Sci. USA 97, 349, 2000), which starts from the 3' end till the last
CATG site of the target cDNA sequence.
Seq primer: M13 forward
FEATURES
Location/Qualifiers
source 1..197
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="human CD15+ myeloid progenitor cells cDNA
library"
/tissue_type="bone marrow"
/cell_type="CD15+ myeloid progenitor cells"
/notes="Organ: thymoid; Vector: PAMPI0; mRNA made from
thymoid carcinoma, cDNA made by oligo-dT priming.
Non-directionally cloned into UDG sites. Size-selected on
agarose gel, average insert size 500 bp. Primary library.
cDNA library preparation: David B. Krizman, Ph.D.
REFERENCE: Krizman et al. (1996) Cancer Research
56:5380-5383."
BASE COUNT 44 a 38 c 37 g 78 t
ORIGIN
Alignment Scores:
Pred. No.: 8,81e-28 Length: 197
Score: 316.00 Matches: 61
Percent Similarity: 98.39% Conservative: 1
Best Local Similarity: 98.39% Mismatches: 1
Query Match: 57,56k Indels: 0
DB: 12 Gaps: 0

US-09-930-312-2 (1-107) x BF942735 (1-197)
Qy 12 PheSerTyrrIlePheSerPheGysSerIleGlnLysThrAlaLeuGlnThrHrGluVal 31
Db 10 TTTCCCTATATTAATGTTCTGTTCCATTCACAAAACCCCTTGCGACCAAGAGTA 69
Qy 32 ArgAsnGysPheGluArgGluValAlaValAsnArgPhePhePheIleValPheSer 51

```

```

Db 70 AGCAATGTTTGGAGAGAGGTGCTGTGCAAAATCGTTCTTTTATAGCTTCTCT 129
Qy 52 AspAlaIleGysTrpIleProValPheValValLysIleLeuSerLeuPheArgValGlu 71
Db 130 GATGCATCTGCTGATCTCTGATTTGTAGTAAATCCTTCCCTCCGCGGAGAA 189
Qy 72 IlePro 73
Db 190 ATACCA 195

RESULT 4
AM436170 235 bp mRNA linear EST 09-JUL-2000
LOCUS 75600 MARC 2P1G Sus scrofa CDNA 5', mRNA sequence.
DEFINITION AM436170
ACCESSION AM436170
VERSION AM436170.1 GI:6971476
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 235)
AUTHORS Fahnenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
JOURNAL EST discovery in swine
COMMENT Unpublished (2000)
CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACCTATGACAT
BACKWARD: GTTTCCTGACGACGACG
Plate: 34 row: F column: 22
Seq primer: ATTTAGTGACATATAG.
Location/Qualifiers
source 1..235
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 49 a 64 c 45 g 77 t
ORIGIN
Alignment Scores:
Pred. No.: 2,04e-24 Length: 235
Score: 288.00 Matches: 55
Percent Similarity: 93.65% Conservative: 4
Best Local Similarity: 87.30% Mismatches: 0
Query Match: 52,46k Indels: 0
DB: 10 Gaps: 0

US-09-930-312-2 (1-107) x AM436170 (1-235)
Qy 45 PhePhePheIleValPheSerAspAlaIleGysTrpIleProValPheValValLysIle 64
Db 8 TTTTCTTTTATAGGTTCTGTGATGCATCTGCTGATTCCTGATTTGTCATTAAT 67
Qy 65 LeuSerLeuPheArgValGluIleProAspTrpMetThrSerTrpIleValIlePhePhe 84
Db 68 CTCTCCCTCTCCGCGGAGAAATACAGGCTCACTCTGCTGCGGCGATTTTTC 127

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Qy 85 LeuProValAsnSerAlaLeuAsnProIleLeuTyrThrLeuThrThAsnPhelys 104  
 |||  
 Db 128 CTTCCGGAGAACAGTGCCTTGAACCAATCTTACACTCTCACACAGCTTTTCAAG 187  
 Qy 105 AsplysLeu 107  
 |||  
 Db 188 GACACGTTG 196

RESULT 5  
 BF021857 456 bp mRNA linear EST 29-DEC-2000  
 LOCUS BF021857  
 DEFINITION UY58n08.y1 McCarrey Eddy round spermatic Mus musculus cDNA clone  
 IMAGE:3663807.5 similar to YR:Q9YVG0 Q9YVG0 CG4187 PROTEIN. ;  
 mRNA sequence.  
 BF021857  
 ACCESSION BF021857.1 GI:10753189  
 VERSION EST.  
 KEYWORDS house mouse.  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 456)  
 REFERENCE  
 AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person  
 , B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurr, R., Ritter  
 , E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterston, R. and Wilson, R.  
 The WashU-NCI Mouse EST Project 1999  
 Unpublished (1999)  
 TITLE  
 JOURNAL CONTACT: Marra M/WashU-NCI Mouse EST Project 1999  
 COMMENT Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MG1:1424575  
 Seq primer: Primer name ambiguous  
 High quality sequence stop: 386.  
 Location/Qualifiers  
 1. 456  
 /organism="Mus musculus"  
 /strain="CD-1"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:3663807"  
 /clone\_lib="McCarrey Eddy round spermatic"  
 /sex="male"  
 /tissue\_type="round spermatids, pooled from multiple mice"  
 /dev\_stage="60 day"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: testis; Vector: pBluescript SK+ (Stratagene  
 ); Site 1: XhoI; Site 2: EcoRI; cDNA oligo dt-primed  
 [5'-(GA)10-ACGTAGCTCGAGTTTCTTTT-3'] and directionally  
 cloned using 5' linkers 5'-AATTCGACGAG-3' and  
 5'-CTGCTCCG-3'. Size selection of >400bp material gives  
 average insert size ranging from 1-2 kb. Library was mass  
 excised (from lambda-UnizAP-XR) and resulting  
 single-stranded phagemids were prepped and transformed  
 into DH10B. Library contains 98.5% recombinants.  
 References: J. Androl. 20:635-639 and Gene 25:263-269.  
 Library constructed and donated by J. McCarrey, Ph.D.  
 (Southwest Foundation for Biomedical Research, Dept. of  
 Genetics); excision done by E.M. Eddy, Ph.D. (National  
 Institutes of Health, National Institute of Environmental  
 Health Sciences). Original lambda-based library is  
 available through ATCC, catalog #63423."

BASE COUNT 120 a 110 c 111 g 115 t  
 ORIGIN  
 Alignment Scores: 2.46e-09 Length: 456  
 Pred. No.:

Score: 162.00 Matches: 30  
 Percent Similarity: 100.00% Conservative: 3  
 Best Local Similarity: 90.91% Mismatches: 0  
 Query Match: 29.51% Indels: 0  
 DB: 12 Gaps: 0

US-09-930-312-2 (1-107) x BF021857 (1-456)

Qy 75 ThrMetThrSerTrpIleValIlePhePheLeuProValAsnSerAlaLeuAsnProIle 94  
 |||  
 Db 40 ACAATACCTCTCTGATGATGTGTTTCTTCCGCGTGAACAGCGCTTAACCCATTC 99  
 Qy 95 LeuTyrThrLeuThrThAsnPhelysAsplysLeu 107  
 |||  
 Db 100 CTTACACTCTGACGACGCTTTTAAAGCAGAGTTG 138

RESULT 6  
 BF632910 574 bp mRNA linear EST 26-OCT-2001  
 LOCUS BF632910  
 DEFINITION RB632910 RIKEN full-length enriched, adult male hypothalamus Mus  
 musculus cDNA clone A230094D06 5', mRNA sequence.  
 BF632910  
 ACCESSION BF632910.1 GI:16469432  
 VERSION EST.  
 KEYWORDS house mouse.  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 574)  
 REFERENCE  
 AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,  
 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda  
 , M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ono, M.,  
 Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki  
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 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,  
 Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
 Unpublished (2001)  
 TITLE  
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 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
 , M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
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 prepare full-length cDNA libraries for rapid discovery of new  
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 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwama, M., Ohara, E.,  
 Matsuhira, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura  
 , S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and  
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 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
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 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamakaki, I., Aizawa  
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 Hayashizaki, Y.  
 Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.  
 e mouse tissues.  
 Location/Qualifiers



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BDGP	Lawrence Berkeley National Lab	
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	Fax: 510 486 6798	
	Email: <a href="http://www.fruitfly.org/EST/estefruitfly.berkeley.edu">http://www.fruitfly.org/EST/estefruitfly.berkeley.edu</a>	
	hit genomic AE003642: arm:2L [13845947,14118016]	
	estimated-cyto:34E1-34F2: 08/23/2001	
	Plate: RH 602 row: E column: 2	
	High quality sequence stop: 540.	
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	/db_xref="taxon:7227"	
	/clone="RH60250"	
	/clone_lib="RH Drosophila melanogaster normalized Head	
	pflc-1"	
	/sex="male and female"	
	/dev_stage="Adult"	
	/lab_host="DHS-alpha Tona"	
	/note="Organ: head; Vector: pPflc1; Site1: XhoI; Site2:	
	BamHI; Library was kindly generated by Piero Carinici at	
	the RIKEN. The library was normalized and excised using	
	Cre recombinase. Plasmid cDNA library."	
BASE COUNT	129 a 148 c 157 g 139 t	
ORIGIN		
Alignment Scores:		
Pred. No.:	6.89e-07	Length: 573
Score:	142.00	Matches: 33
Percent Similarity:	52.38%	Conservative: 22
Best Local Similarity:	31.43%	Mismatches: 40
Query Match:	25.87%	Indels: 10
DB:	13	Gaps: 3
US-09-930-312-2 (1-107) x B1630907 (1-573)		
QY	2 ValaAsnLeuAlaPheLeuIleValaPheSerTyrlerThmetPheCysSerIle 21	
Db	26 ATCAAGGAGTGGCGATTTCTCAGCTCTGATGGGTGCTCTCAAGATGACTGGGCCATA 85	
QY	22 Gln--LysThrAlaLeuGlnThrThrGluValArgAsnGlyArgGluValAla 40	
Db	86 AGGGGACACCGACGGCATGTGACACAGATATTCGCGA----- 121	
QY	41 ValAlaAsnArpPhePhePheIleValPheSerAlaIleCysTrpIleProValPhe 60	
Db	122 ATTGCCAGACGCAATGGCTGTGTGCTTTACTACTGCTTCCTGCTGGTGCACCTATCGCC 181	
QY	61 ValValLysIleLeuSerLeuPheArgValGluIleProAspThrMetThrSerTrpIle 80	
Db	182 TTCCTTCGACACCTGCGCATTTGGCCCTGCGCAACGATTTGCTGCAGAGCGCAAGATC 241	
QY	81 --ValIlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrlerThr 99	
Db	242 TTTACGGATTTGGCTGCTCCCTTGATATGTTGCTGCAATCCCTTTCTACGCCAATATG 301	
QY	100 ThrAsnPhePheLys 104	
Db	302 ACCAAGCAGTTCAG 316	
RESULT 8		
B1628622		
LOCUS	B1628622	
DEFINITION	B1628622 610 bp mRNA linear EST 10-SEP-2001	
	RH57122.5prlme RH Drosophila melanogaster normalized Head pflc-1	
	Drosophila melanogaster cDNA clone RH57122.5 similar to rk:	
	Pan0008930 GO: [plasma membrane (GO:0005886)]; G protein linked	
	receptor (GO:0004930); G protein (GO:0004930); G protein linked	
	located on: 2L 34E2-34E2:: 08/22/2001, mRNA sequence.	
ACCESSION	B1628622	
VERSION	B1628622.1	
KEYWORDS	EST.	
SOURCE	fruit fly.	

	ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelecygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Phytozoidea; Drosophilidae; Homophyllia.
	REFERENCE	1 (bases 1 to 610)
	AUTHORS	Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson, J., Champe,M., Chavez,C., Dorset,V., Farfan,D., Frise,E., George, R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nuno,J., Pacleb,J., Pargas,V., Park,S., Poulsenavong,S., Wan,K., Yu,C., Lewis,S.E., Celisner,S. and Rubin, .G.M. BDGP/HMI RH Drosophila EST Project Unpublished (2001) Contact: Stapleton, M. BDGP
	TITLE	Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu hit genomic AEO03642: arm:2L [13845947..14118016] estimated-cyto:34E1-34F2: 08/22/2001 Plate: RH.571 row: B column: 10 High quality sequence stop: 539e.
	FEATURES	Location/Qualifiers  1..610 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /cclone="RH571122" /cloned_lib="RH Drosophila melanogaster normalized Head pfic-1" /sex="male and female" /dev_stage="Adult" /lab_host="DH5-alpha Tona" /note="Organ: head; Vector: pfic1; Site_1: XhoI; Site_2: BaamHI. Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
	BASE COUNT	143 a    160 c    166 g    139 t    2 others
	ORIGIN	
	Alignment Scores:	
	Pred. No.:	7.33e-07 Length: 610
	Score:	142.00 Matches: 33
	Percent Similarity:	52.38% Conservative: 22
	Best Local Similarity:	31.43% Mismatches: 40
	Query Match:	25.87% Indels: 10
	DB:	Gaps: 3
OY	-US-09-930-312-2 (1-107) x BR628622 (1-610)	
OY	2 ValmsnleueAlaphellelleValpheserTyrllehmerhphecysseile 2t	::::                    ::::                    ::::
Db	26 ATCAACGGATCGCATTCCTACTGTAGTGTTGCCATTGAAGTAGTGGCCATA 85	: :                     : :                     : :
OY	22 glN---lystrhalaleauglnrthrHgLuvalAAsncypheglayrgluValala 4o	:::    - - - l y s t r h a l a e u g n i r t h r H g U v a l A A s n c y p h e g l a y r g l u V a l a l a
Db	86 AGGGCAGCACGCATGACAACAAATGATTCGGA----- 12l	: : :                     : :                     : :
OY	41 ValalalsnaatargphepnehellavalphaseraspalielcystripplierProvalphe 6o	: : :                     : : ~~~~~~ : :                     : :
Db	122 ATTGCAACGAGCAATGGCTGTGTGGTCTTACGTGACTTCCTGTGGTGCACCATTACGCC 18l	: : :                     : : ~~~~~~ : :                     : :
OY	61 ValVallylsilleusserLeupeharVaGlUileroasPhmrhetrhserPlie 8o	V a l V a l l y l s i l l e u s s e r L e u p e h a r V a G l U i l e r o a s P h m r e t r h s e r P l i e
Db	182 TTCCTTCGATCATCGCATCTTGGCCCTGCMACTGATTTCCGTGGAGCAGGCCAAGATC 24l	: : :           : : :           : : :           : : :
OY	81 ---VallliepbeleuproValasnSerAlaleuasnProlleuleutyrrhlreuthr 99	-- -- V a l l l e p b e l e u p r o V a l a s n S e r A l a l e u a s n P r o l l e u l e u t y r r h l r e u t h r
Db	242 TTTAAGGATATTGGTGCCCTTGTAATGATGTCTGCAATCCCTTCTCTACAGCCATAATG 30l	: : :                     : : :                     : : :
OY	100 Thrashnephelys 104	
Db	302 ACCAACGAGGATTCAG 316	

[illegible]

SOURCE Ciona intestinalis.  
ORGANISM Ciona intestinalis  
COMMENT Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.  
REFERENCE 1 (bases 1 to 522)  
AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.  
TITLE Expressed genes in Ciona intestinalis  
JOURNAL Unpublished (2000)  
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FEATURES  
source 1..522  
/organism="Ciona intestinalis"  
/db\_xref="taxon:7719"  
/clone="c1b39n21"  
/clone\_lib="Nori Satoh unpublished cDNA library, tailbud embryo"  
/tissue\_type="whole animal"  
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BASE COUNT 121 a 122 c 127 g 152 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2,12e-06 Length: 522  
Score: 137.50 Matches: 26  
Percent Similarity: 52.08% Conservative: 24  
Best Local Similarity: 27.08% Mismatches: 45  
Query Match: 25.05% Indels: 1  
DB: 10 Gaps: 1

US-09-930-312-2 (1-107) x AV995043 (1-522)

QY 3 AsnLeuLeuAlaPheLeuLeuLeuAlaPheSerTyrIleThrmethPhecysSerIleGln 22  
||| |||||: : : |||||: : : : :  
Db 79 AATTATACCGCGTTGTGTTGTCGTCATCATCATCATCATCATCAAGCGCGT 138  
QY 23 LysThrAlaLeuGln--ThrThrGluValAlaArgAsnCysPheGlyArgGluValAlaVal 41  
: : : |||||: : : : : : : : : : : :  
Db 139 CCATACGCGATCAGCTTCATATCATCTCCAGCGGTATGCTACACATAGACCATG 198  
QY 42 AlaAsnArgPhePhePheLeuAlaPheSerAspAlaIleCysTrpIleProValPheVal 61  
: : : : : : : : : : : : : : : : : :  
Db 199 CAAGAGAGATCATCATGATTAACTGCACCGACTTTGTGTGGGTCCTCCATCTCCATC 258  
QY 62 VallysIleLeuSerLeuPheArgValGluIleProAspThrmetPheSerTrpIleVal 81  
: : : : : : : : : : : : : : : : : :  
Db 259 ACAGTCTTCTGAGGTTTAGCGGCATCGAGGTTCCCGATATCATGTACCGGCTGTCCG 318  
QY 82 IlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThr 97  
: : : |||||: : : |||||: : : |||||: : : : :  
Db 319 GTCGTCCTCTCCCGCTGAATTCGCGCGTGAACCGCATCTTACTTCG 366

RESULT 11  
AV883650 585 bp mRNA linear EST 08-NOV-2001  
LOCUS AV883650/c  
DEFINITION intestinalis cDNA clone rcltb39n21 3', mRNA sequence.  
ACCESSION AV883650  
VERSION AV883650.1 GI:16871174  
KEYWORDS EST.  
SOURCE Ciona intestinalis.  
ORGANISM Ciona intestinalis  
REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.  
AUTHORS 1 (bases 1 to 585)  
TITLE Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.  
Expressed genes in Ciona intestinalis

JOURNAL Unpublished (2000)  
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FEATURES  
source 1..585  
/organism="Ciona intestinalis"  
/db\_xref="taxon:7719"  
/clone="rcltb39n21"  
/clone\_lib="Nori Satoh unpublished cDNA library, tailbud embryo"  
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/dev\_stage="tailbud embryo"  
/note="Vector: pBluescript SK"

BASE COUNT 175 a 137 c 132 g 141 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.37e-06 Length: 585  
Score: 137.50 Matches: 26  
Percent Similarity: 52.08% Conservative: 24  
Best Local Similarity: 27.08% Mismatches: 45  
Query Match: 25.05% Indels: 1  
DB: 10 Gaps: 1

US-09-930-312-2 (1-107) x AV883650 (1-585)

QY 3 AsnLeuLeuAlaPheLeuLeuLeuAlaPheSerTyrIleThrmethPhecysSerIleGln 22  
||| |||||: : : |||||: : : : :  
Db 503 AATTATACCGCGTTGTGTTGTCGTCATCATCATCATCATCAAGCGCGT 444  
QY 23 LysThrAlaLeuGln--ThrThrGluValAlaArgAsnCysPheGlyArgGluValAlaVal 41  
: : : |||||: : : : : : : : : : : :  
Db 443 CCATACGCGATCAGCTTCATATCATCTCCAGCGGTATGCTACACATAGACCATG 384  
QY 42 AlaAsnArgPhePhePheLeuAlaPheSerAspAlaIleCysTrpIleProValPheVal 61  
: : : : : : : : : : : : : : : : : :  
Db 383 CAAGAGAGATCATCATGATTAACTGCACCGACTTTGTGTGGGTCCTCCATCTCCATC 324  
QY 62 VallysIleLeuSerLeuPheArgValGluIleProAspThrmetPheSerTrpIleVal 81  
: : : : : : : : : : : : : : : : : :  
Db 323 ACAGTCTTCTGAGGTTTAGCGGCATCGAGGTTCCCGATATCATGTACCGGCTGTCCG 264  
QY 82 IlePhePheLeuProValAsnSerAlaLeuAsnProIleLeuTyrThr 97  
: : : |||||: : : |||||: : : |||||: : : : :  
Db 263 GTCGTCCTCTCCCGCTGAATTCGCGCGTGAACCGCATCTTACTTCG 216

RESULT 12  
BB553437 676 bp mRNA linear EST 26-OCT-2001  
LOCUS BB553437  
DEFINITION BB553437 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330007C19 3', similar to M81310 Mouse lutealizing hormone receptor mRNA, mRNA sequence. ;  
ACCESSION BB553437  
VERSION BB553437.2 GI:16448285  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 676)  
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL  
COMMENT

Unpublished (2001)  
On Aug 1, 2000 thi

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Cardinacci, P., Shioda, I., Hayatsu, N., Suganara, I., Shioda, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normal fibroblast and epithelial cell lines derived from human tumors.



